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Listing first 45 summaries
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2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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AAH20174
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AAH20182
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AAS42107
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1579.785 Million cell updates/sec
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|------------|--------------------|-----------|----------|---------------|----------|----------|----------|---|-------------|--------------------|-----------|----------|----------|--------------------|--------------------|------------|----------|----------|-------------|--------------------|--------------|-------------|-------------|----------|----------|--------------------|--------------------|----------|--------------------|--------------------|--------------------|----------|----------|-----|--------------------|----------|--------------------|
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| | 8 | 588 | 4 | 3054 | 2581 | 2552 | 2166 | 2024 | 378 | 725 | 725 | 466 | 466 | 466 | 466 | 466 | 466 | 466 | 466 | 466 | 466 | 3086 | 3078 | 3073 | 3002 | 2362 | 804 | 41599 | 2341 | 3631 | 1830121 | 3080 | | 85 | \vdash | 14 | 0 |
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| ALIGNMENTS | ABZ41770 | ABZ41332 | ABV47128 | ABS70481 | AAQ70104 | AA188906 | AAF86585 | AAC81718 | AAK63709 | ABS76832 | ABS76828 | ABX16976 | ABX64012 | ABX79373 | ABX77777 | ABX90166 · | ABX81076 | ABX80693 | ABX80189 | AAF44124 | AAZ64978 | AAK52602 | AAK51618 | ACC46483 | AAZ43957 | AAH18260 | AAH08436 | AAZ35351 | AAX82193 | ABL10204 | AAT42063 | ABL28356 | ABV53300 | 550 | 970 | ABQ75995 | ABS79021 |
| | N. gonorrhoeae nuc | norrhoeae | | $\overline{}$ | O | | | | າ immune/ha | Frog embryonic gen | embryonic | PRO | | Human sectreted/tr | Human PRO polynucl | | | = | human secre | Human EST DNA16829 | ane-bound pr | polynucleot | polynucleot | | | Human cDNA sequenc | Human cDNA clone (| Ω | Influenza virus PB | Drosophila melanog | Haemophilus influe | _ | prostate | | Sheep BSE-resistan | ס | E. coli CFT073 gen |

09-AUG-2001 (first entry) AAH20176; AAH20176 standard; DNA; 12792 BP. Human mutated spastin nucleotide sequence SEQ ID NO:7.

Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell; abnormal neuronal lipid storage; genetic disorder; characterisation; ds domo sapiens.

Synthetic.

WO200129266-A2. 26-APR-2001. 77..6604 Location/Qualifiers /*tag= a /product= "mutated spastin" /*tag=

20-OCT-2000; 2000WO-US29130

9908-0160588

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RESULT 2
AAH20174
ID AAH2
XX
AC AAH2
XX
AC AAH2
XX
DT 09-1
XX
DE Humm
XX
KW aut,
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Best Local :
Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saquenay; mutat neurodegenerative disease; reduced sensory nerve conduction; dia reduced motor nerve velocity; hypermyelination of retinal nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        abhormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disease or disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with spastin
                                                                                                            Human spastin
                                                                                                                                                     09-AUG-2001
                                                                                                                                                                                              AAH20174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein or spastin gene expression or activity. The present sequence encodes a mutated human spastin.

N.B. The present sequence is not given in the present specification is derived from the human spastin nucleotide sequence (AAH20174) as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
                                                                                                                                                                                                                                AAH20174 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12792 BP; 4163 A; 2256 C;
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                                                                                                                                                                                                                                                                                                                                      AATACAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAACA
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                                                                                                       nucleotide sequence
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Pred. No. 5.4e-23;
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                                                                                                       ID NO:1
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                                         mutation;
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diagnosis;
rve fibre;
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                                                                                                                                                                                                                                                                                                                                            acid molecule in a sample. (I) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease comprises reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and abnormal neuronal lipid storage. (I) can also be used to produce antisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of the corresponding protein is expressed.
                                                                                                                                                                                                                    Sequence 12793 BP;
                                                                                                                                                                                                                                                       having or at risk of developing a disorder associated with sprotein or spastin gene expression or activity. The present encodes human spastin as given in the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy and as a spastin polypeptide agonists. (I), their fragments or their complements can be useful for assaying the presence of a nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
                                                                                                                                                                                                                                                                                                               or activity of (I).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hudson TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000; 2000WO-US29130
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(HOPI-) HOPITAL SAINTE-JUSTINE.
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                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                            developing a disease or disorder associated with aberrant expression activity of (I). The assays can be utilised to identify a subject ving or at risk of developing a disorder associated with Spastin
6603
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DB; AAB97819.
                                61 AATACAGTTAAAAAAACGGTATTTCCCTGGTT
                                                                                      1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT
                                                                                                                                             69;
                                                                                                                                                                Similarity
TAATACAGTTAAAAAAACGGTATTTCCCTGGT
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                                                                     GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTTGAATTGC
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                                                                                                                                               Conservative
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                                                                                                                                                                                                                    4163 A; 2256 C;
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75.0%;
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0;
                                                                                                                                                                Score
Pred.
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                                                                                                                                                                                                                      3887 T; 0 other;
                                                                                                                                                                                 22;
                                                                                                                                             Indels
                                                                                                                                                                               Length 12793;
                                                                                                                                             0;
                                                                                                                                           Gaps
                                                                     6602
                                                                                                        60
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0;

autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis;

spastin; ARSACS; chromosome 13q11;

identification,

spastin nucleotide sequence

SEQ ID

NO:11

reduced

Human mutated

mouse;

09-AUG-2001 (first entry)

AAH20178 standard; DNA;

12793

ВÞ

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AAH20178
IID AAH2
XX AAH2
XX AAH2
XX OAH2
XX OAH2
XX OAH2
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XX Huma
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                                                                                                                                                                                                              The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in gene therapy and as a spastin polypeptide agonists. (I) their fragments or their complements can be useful for assaying the presence of a nucleic acid molecule in a sample. (I) is useful for diagnosing or alding in the diagnosis of an early onset neurodegenerative disease in an individual. The neurodegenerative disease reduced sensory nerve conduction, reduced motor nerve velocity, hypermyelination of retinal nerve fibres, atrophy of upper cerebellar vermis, absence of Purkinje cells and cannormal neuronal lipid storage. (I) can also be used to produce annisense nucleic acids, is useful as molecular weight or chromosome markers, to identify genetic disorders, as hybridisation probes or primers, as an antigen, identify and express recombinant protein for analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from the present invention can be used to identify subjects having or at risk of developing a disorder associated with aberrant expression or activity of (I). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin corresponds or protein or spastin gene expression or activity. The present sequence is not given in the present specification but is derived in name spastin nucleotide sequence (AAH20174) as
                                                                    Query Match
      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
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(HOPI-) HOPITAL SAINTE-JUSTINE
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of upper cerebellar vermis; absence of Purkinje cell;
l neuronal lipid storage; genetic disorder; characterisation; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page -;
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                                                                                                                                      2255 C; 2487 G; 3888 T;
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Score 55.2; DB 22
Pred. No. 8.9e-08;
0; Mismatches 23
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RESULT 4
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                                          CC chromosome 13q11. (1) have neuroprotective activities and can be used in CC gane therapy and as a spastin polypeptide agonists. (1), their fragments CC or their complements can be useful for assaying the presence of a nucleic CC acid molecule in a sample. (1) is useful for diagnosing or aiding in the diagnosis of an early onset neurodegenerative disease in an individual. CC The neurodegenerative disease comprises reduced sensory nerve conduction, CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of Purkinje cells and CC abnormal neuronal lipid storage. (1) can also be used to produce CC antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC primers, as an antigen, identify and express recombinant protein for canalysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC the present invention can be used to identify subjects having or at risk of facularions a disease or diseased to identify subjects having or at risk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; mouse; spastin; ARSACS; chromosome 13q11; identification; autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell; abnormal neuronal lipid storage; genetic disorder; characterisation; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spastin
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page -;
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                                                                                                                                                                                                                                                                                                                            (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in
                                                                                                                                                                                                                                                                                                                                                                   present invention describes human and mouse spastin, and mutated an spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay
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of developing a disease or disorder associated with aberrant or activity of (I). The assays can be utilised to identify a

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The present invention describes human and mouse spastin, and mutated human spastin (autosomal recessive spastic ataxia of Charlevoix-Saguenay (ARSACS)) gene sequences (I). The spastin gene has been mapped to chromosome 13q11. (I) have neuroprotective activities and can be used in
                                                                 Claim 1;
                                                                                          gene
                                                                                                 New isolated polynucleotide, encoding spastin gene, and polypeptides, useful for diagnosing autosomal recessive spastic ataxia of Charlevoix-Saguenay disease by detecting two point mutations in spast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   autosomal recessive spastic ataxia of Charlevoix-Saguenay; mutation; neurodegenerative disease; reduced sensory nerve conduction; diagnosis; reduced motor nerve velocity; hypermyelination of retinal nerve fibre; atrophy of upper cerebellar vermis; absence of Purkinje cell;
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        (UYMC-) UNIV MCGILL.
(HOPI-) HOPITAL SAINTE-JUSTINE
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Pred. No. 8.9e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6634
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                                                                                                                                                                                                                                                                                                                                                                              mutation;
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RESULT 7
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ID AAS42
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AC AAS4
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DT 17-C
DT 17-C
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WALL
DT 11-1-C
DT 11-C
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Huma
DE Huma
KW Liga
KW L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C chromosome 13q11. (I) have neuroprotective activities and can be used in C gene therapy and as a spastin polypeptide agonists. (I), their fragments CC or their complements can be useful for assaying the presence of a nucleic card molecule in a sample. (I) is useful for diagnosing or adding in the C diagnosis of an early onset neurodegenerative disease in an individual. CC reduced motor nerve velocity, hypermyelination of retinal nerve fibres, CC atrophy of upper cerebellar vermis, absence of purkinje cells and CC abnormal neuronal lipid storage. (I) can also be used to produce CC antisense nucleic acids, is useful as molecular weight or chromosome CC markers, to identify genetic disorders, as hybridisation probes or CC primers, as an antigen, identify and express recombinant protein for CC analysis, characterisation or therapeutic use, or as markers for tissues in which the corresponding protein is expressed. Diagnostic methods from CC in which the corresponding protein is expressed. Diagnostic methods from CC in the present invention can be used to identify subjects having or at risk of a protein can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used to identify subjects having or at risk can be used
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Best Local
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                                                                                                                         numan; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of developing a disease or disorder associated with aberrant expression or activity of (1). The assays can be utilised to identify a subject having or at risk of developing a disorder associated with Spastin protein or spastin gene expression or activity. The present sequence encodes mouse spastin as given in the present invention.
                                                                                                                                                                                                                                                                                              Genomic sequence #423 encoding novel human enzyme polypeptide.
                                                                                                                                                                                                                                                                                                                                                 17-DEC-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAS42107 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11493 BP; 3599 A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene sequence
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                                                                                                                                                                                                                                                                                                                                                                                                    AAS42107;
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02-AUG-2001.
                                              WO200155301-A2
                                                                                         Homo sapiens.
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DB; AAB97820.
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Pred. No. 2.8e-07;
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22-AUG-2000
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18-AUG-2000;
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07-JUL-2000;
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               CA,
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              Barash SC,
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2000US-0236370.
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptides (AAU22015-AAU23814), and the CDNA and genomic sequences of cencoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, ci isomerases or ligases. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of a wide range of celargnosis, treatment, prevention and/or prognosis of a wide range of continuous control of the invention and/or prognosis of a wide range of celargnosis, including hyperproliferative disorders (e.g. cancer), continuous control of the control of the invention can also be used in gene therapy.

Control of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy. Chasties of the invention can also be used in gene therapy.
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Matches 56
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                                                                                                                                                                                                                                                                                                                                                                     Human; tyrosine phosphatase subfamily; cellular process modulation; phosphatase; chromosome 14; single nucleotide polymorphism; SNP; variant; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous
                                            variation
                                                                                                                          variation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                              / tag= a
/product= "Human phosphatase protein"
replace (3114, A)
/*tag= b
                       replace (4514,
/*tag= d
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/note= "Polymorphic site 2"
replace (4514, G)
                                                                                                    replace (4004,
/*tag= c
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/note= "Polymorphic site 1"
/standard_name= "Single nucleotide polymorphism (SNP)"
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     552 A;
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62.9%;
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Pred. No. 0.066;
0; Mismatches
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                /standard_name= "Single nucleotide
/note= "Polymorphic site 19"
replace (28030, G)
/*tag= w
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/*tag= v
                                                                                                                                                                                                                               /standard_name= "Single nucleotide /note= "Polymorphic site 13" replace (20988, -)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /standard_name= "Single nucleotide
/note= "Polymorphic site 7"
replace (16586, T)
/*tag= i
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replace (20999, T)
                                                                                                                                                                                                                                                                                                                                    /standard_name= "Single nucleotide
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replace (18518, A)
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/note= "Folymorphic site 8"
replace (16644, C)
/*tag= j
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/note= "Polymorphic site 6"
replace (14523, C)
/standard_name= "Single nucleotide
/note= "Polymorphic site 20"
                                                                                           /standard_name= "Single nucleotide
/note= "Polymorphic site 17"
replace (26291, T)
                                                                                                                           /standard_name= "Single nucleotide
/note= "Polymorphic site 16"
replace (21625, T)
                                                                                                                                                             /standard_name= "Single nucleotide
/note= "Polymorphic site 15"
/eplace (21465, G)
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/note= "Polymorphic site 12"
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/note= "Polymorphic site 10"
replace (18117, T)
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/note= "Polymorphic site 9"
replace (17969, G)
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/note= "Polymorphic site 5"
replace (11897, C)
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/note= "Polymorphic site 4"
replace (11672, G)
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replace (7570, G)
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                      New phosphatase peptide for the treating related disorders -
                                                 P-PSDB;
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                                                                                          (PEKE )
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11-OCT-2000;
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DB; AAE08552.
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2000US-0685853
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/*tag= ae

40039..45810

/*tag= af

45811..45871
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57603..57761
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47134.
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47003.
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/note= "Polymorphic site 23; This position is given
as 39269 in the specification"
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/note= "Polymorphic site 22"
replace (39263, G)
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/*tag= x
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/note= "Polymorphic site 21"
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The present invention relates to polynucleotide sequences from the genome of the pathogenic Escherichia coli strain CFT073. Almost all the sequences present in E. coli CFT073 are absent in the previously sequenced laboratory strain K-12. The polynucleotide sequences of the invention are useful for preventing, diagnosing or treating E. coli CFT073 infection in humans or livestock. The polynucleotide sequences are useful for preventing urinary tract infections and pyelonephritis. Likewise, the polypeptides encoded by the different open reading frames (ORF1-5) are useful for generating a vaccine against uropathogenic E. coli strains. ABS78834-ABS79085 represent
                                                                                                                                                                                                                                                                                                           Claim 1; Page 566; 765pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention provides phosphatase peptides, proteins and their polynucleotides. The phosphatase proteins are related to the protein tyrosine phosphatase subfamily. The peptides of the invention are useful for identifying a modulator of phosphatase peptide expression. Modulators of phosphatase peptide are useful for treating diseases or conditions mediated by a human phosphatase protein. The phosphatase gene of the present invention can be expressed in yeast to identify possible interactors and substrates. Artificially synthesised enzymes or derived peptides can be used to activate or inhibit cellular processes modulated by this phosphatase. The present sequence is a human gene encoding phosphatase protein. This gene is located on human chromosome 14.
                                                                                                                                                                                                                                                                                                                                                                                                             useful for
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No. 0.14;
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13

Matches Query Match Best Local

Local

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Score 29.4; E Pred. No. 17; 0; Mismatches

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RESULT 10
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XX Sheep PrP
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KW breeding;
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                                                                             prion protein genes, involving comparing a nucleic acid sequence with a reference. The method is used for determining the PrP allele in an animal (or human) in order to assess susceptibility to transmissible spongiform encephalopathies (TSE), most especially scrapic in sheep. This assists in the selection, for breeding, of animals having the alleles known to be associated with lowest risk. The method is reproducible and rapid, provides high resolution between allelic variants and is suitable for processing large numbers of samples. The current sequence represents a sheep PrP gene, that is used in the context of the invention as a
                                                         comparison
                                                                                                                                                                                                                                                                                                                                   The invention relates to an assay for determining allelic variations
                                                                                                                                                                                                                                                                                                                                                                                             Claim 2 (i)(a); Fig 1; 36pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Assay for comparing nucleic acid sequence with a reference, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N
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58; Conservative
     31412 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bowles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1604
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; DNA; 31412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATACAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAACA 103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                selection;
                                                            nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    prion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2001GB-0000702
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  8889 A; 6517 C; 6464 G;
                                                         acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      coli strain CFT073
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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  9542 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encephalopathy; TSE; scrapie;
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RESULT 11
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PN W02
XX W02

RESULT 12
ABS55500/c
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                                                                                                                                                                                                            Matches '
                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                           The invention relates to a novel transgenic bovine/cervid comprising a transgene encoding a mutant prion protein (PrP) polypeptide, in which a substitution has been made at position 171 of the sequence, which renders the bovine/cervid resistant to bovine spongiform encephalopathy (BED) and transmissible spongiform encephalopathy (TSE) disease, respectively. The transgene of the invention has neuroprotective activity. The method is useful for producing a transgenic bovine or cervid resistant to BSE and TSE diseases. The bovine prion gene is useful for producing transgenic cattle exhibiting resistance to bovine spongiform encephalopathy. The sequence represents the transgene encoding the mutant PrP polypeptide in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transmissible spongiform encephalopathy; neuroprotective; prion protein; bovine spongiform encephalopathy; transgenic; BSE; bovine; cervid; PrP; TSE; gene; ss; sheep.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New transgenic bovine and cervid useful for producing animals which are resistant to bovine spongiform encephalopathy and transmissible spongiform encephalopathy disease, comprise a transgene encoding a mutant PrP polypeptide -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               )702/c
ABV99702 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-092895/08.
P-PSDB; ABP57901.
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                                                                                                                                                                                                                                                                               Sequence 31412 BP; 8889 A; 6517 C; 6464 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 84-93; 98pp; English.
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                                                                     21543 TCAAAGGAATT 21533
                                                                                                                                                         13 ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                                                                                                                                                                                                               45;
                                                                                                                                                                                                                                Similarity
                                                                                                                                      AAAACGGTATT
                                                                                                      AAAACGGTATT 83
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nilarity 63.4%;
Conservative
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                                                                                                                                                                                                            Score 29.4; E
Pred. No. 17;
0; Mismatches
                                                                                                                                                                                                                                              DB 25;
                                                                                                                                                                                                                                                                                 9542 T; 0 other;
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 /*tag= ag
/standard_name= "S
replace (5126, T)
/*tag= ar
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135589..135601
/*tag= ab
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/number= 12
                                          /standard_name= "Single replace (5037, A)
                                                                         /standard_name= "Single replace (4651, C)
                                                                                                         replace (4345,
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replace (2011, C)
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replace (1131, A)
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replace (210, A)
/*tag= ai
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135602..137397
/*tag= ac
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/*tag= v
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132923..133775
                                                                                                                  /standard_name= "Single
                                                                                                                                       ceplace (4309, C)
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**tag= w
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*tag= aa
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37527..145751
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37398..137526
*tag= ad
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'tag= ah
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RESULT 13
ABV53300
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                     ABV53300 standard; cDNA; 594
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                                                                                      CAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAAC
                                                                                                                  TGCATTGCATTATATTGTATAATCACCATTAATATTTTCTTTTTTGCCTGAATTGCTCACT 73626
                                                                                                                                      TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA
                                                                                                                                                          28.3%;
ilarity 56.1%;
Conservative
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replace (10594, (
/*tag=__bi
                                                                                                                                                                                                   /standard_name= "Single nucleotide replace (11233, T)
/*tag= bj
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replace (9471, G)
/*tag= bg
/standard_name= "Single |
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replace (7339, G)
/*tag= bd
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replace (6048, T)
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/*tag= bh
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replace (6382, T)
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replace (6228..6229, C)
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148567 0;

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17-SEP-2002

(first entry)

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RESULT 14
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16-MAR-2000;
25-MAY-2000;
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 10326; 11750pp; English.
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18-JUL-2000;
  26-MAR-2002
                              ABL28356
                                                      ABL28356 standard;
                                                                                                                                                                                                                                                                                              Sequence

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastazed in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

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                                                                                                                                                    AATACAGTTAAAAAAACGGTATTTC 85
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2000US-207454P.
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 (first entry)
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2000US-219007P.
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                                                        DNA;
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                                                                                                                                                                                                                                      Score 29; DB Pred. No. 11; 0; Mismatches
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RESULT 15
AAT42063/c
ID AAT42
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XX AAT42
XX I4-SE
DT 14-SE
DT 14-SE
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XX Genom
XW Genom
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W09633276-A1

Haemophilus influenzae

Genome; bacterium; Haemophilus influenzae; expression modulating fragment; regulation; organism; open reading frame; ORF; ds.

Haemophilus influenzae complete

genome sequence

computer readable medium;
; gene expression; vector;

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Query Match
Best Local S
Matches 44
                                                  2063/c
AAT42063
                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL10176-ABL30511), expressed DNA sequences (ABL01840-ABL6175) and the encoded proteins
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                         AAT42063;
                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 36541; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid genes from Drosophila and
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11-JUL-2000;
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pharmaceutical; gene; ds.
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14-SEP-1999
                                                                                                                                                                                                                                                                                                               The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   interactions
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                 ftp.wipo.int/pub/published_pct_sequences.
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2000US-0614150
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(first entry)
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RESULT 16
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21-APR-1995;
07-JUN-1995;
                            23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                       WO200171042-A2
                                                                                                                                                                                                                                                   Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster expressed polynucleotide SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            readable medium (CRM) having recorded upon it the complete H.influenzae nucleotide sequence (I), a representative fragment of (I) or a nucleotide sequence at least 99% identical to (I). By providing the full-length genomic sequence in a computer readable form, it is possible to identify commercially important nucleic acid fragments and expression modulating fragments (EMFs) of the Haemophilus genome. The EMFs can be used to regulate the expression of a nucleic acid molecule. Vectors and altered organisms comprising the predicted ORFS can be used to produce any of the polypeptide fragments of the H. influenzae Rd genome.
                                                                                                     23-MAR-2001;
                                                                                                                                                   27-SEP-2001
                                                                                                                                                                                                                                                                                                                            Drosophila;
                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Haemophilus influenzae Rd genome medium - useful for identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-485782/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Adams
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTAAAGAGTCGTTATTTCCATAATAGTTAGTTGATGTATTATTTCCATTTTCATTTAAT 1541172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fleischmann RD,
                                                                                                                                                                                                                                                                                                                         developmental biology;
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                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                         2000US-191637P
2000US-0614150
                                                                                                     2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents the complete genome sequence of the bacterium of luenzae strain Rd. The invention relates to a computer
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95US-0426787.
95US-0476102.
                                                                                                                                                                                                                                                                                                     gene;
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Pred. No. 59;
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                                                                                                                                                                                                                                                                                                                       cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Venter JC,
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y important nucleio
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RESULT 17
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                     Cold-adapted influenza viruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA protein; NP protein; M protein; vaccine; flu; influenza; ss.
                                                                    WPI; 1999-385377/32.
                                                                                                                                        Cheoun
                                                                                                                                                                                                                                                                         30-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                  WO9928445-A1
                                                                                                                                                                                                                                                                                                                                                                                                          Influenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cold-adapted influenza virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza virus PB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX82193 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3631 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequences (ABL01840-ABL16175) and the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   genes from Drosophila and interactions -
                                                                                                                                                                               (CHEI-) CHEIL JEDANG
                                                                                                                                                                                                                            29-NOV-1997;
                                                                                                                                                                                                                                                                                                                     10-JUN-1999
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59.0%;
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                                                                                                                                   Kim
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Pred. No. 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВP
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protein;
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sensitivity;
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vaccines against

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Y T T X R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R R X R X R X R X R R X R X R R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R X R 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Diagnosing and determining prognosis for cancer with derangements of chromosome 9p21 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           methylthioadenosine phosphorylase; glioma; primary lymphoid malignancy; non-small cell head and neck cancer; ovarian cancer; bladd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to cold-adapted influenza viruses prepared by passage culture of A/x-31, B/Yamagata/16/88 or B/Lee/40 viruses at low temperatures. A cDNA gene of cold-adapted influenza virus HTCA-A101 can be selected from a group consisting of PB2 protein gene, PB1 protein
                                                                                                                                                                                                                                                                                                 23-JUN-1998;
17-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chromosome 9p21; human; cancer; tumour; diagnosis; prognosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27-MAR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ35351 standard; DNA; 41599 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2341 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; Page 52-53; 62pp; English
                                                                                                      WPI; 2000-126650/11.
                                                                                                                                                                                                                                    (REGC ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                    21-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9967634-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chondrosarcoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cosmid including sequence spanning human chromosome 9p21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expected. The present sequence represents the influenza virus PB1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2292 AAAATAGTGAATTTAGCTTGTCCTTCATGAAAAA 2325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10 GGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTT 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 AAAAAACGGTATTTCCCTGGTTCTGATCCAACA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                   DA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAAGAAGAGTTCACTGAGATCATGAAGATCTGTTCCACCATTGAAGAGCTCAGACGGCA 2291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                               Schmid M,
                                                                                                                                                                                                                                    CALIFORNIA
                                                                                                                                                                                                                                                                                                 98US-0090411.
99US-0335231.
                                                                                                                                                                                                                                                                                                                                                                                                99WO-US13981.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.6%;
                                                                                                                                                                   Carrera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 28.4; DI
Pred. No. 22;
0; Mismatches
                                                                                                                                                                   G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         oma; melanoma;
cell lung cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41;
                              causitively associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Matches

50;

Conservative

0

Mismatches

36;

Indels

0;

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Query Match
Best Local
                                                                             Sequence 41599 BP; 13477 A; 8216 C; 8242 G; 11664 T; 0 other;
                                                                                                                                                        are provided for use in claimed methods for diagnosing and determining a prognosis for cancer associated with derangements of 9p21, especially a glioma, primary lymphoid malignancy, non-small cell lung cancer, melanoma, head and neck cancer, ovarian cancer,
                                                                                                                                                                                                                                                      9921 region centromeric to SRS 3.21 are deleted, where a positive finding in step (b) are indicative of a cancer in an early stage of tumour development and a positive finding in step (a) is indicative of a cancer in an advanced stage of tumour development.

Primer pairs (see AAZ35354-75)
                                                                                                                                                                                                                                                                                                                                                                  by determining whether (a) portions of the 9p21 region including and telomeric to STS 3.21 are deleted, and (b) portions of the 9p21 region centromeric to SRS 3.21 are deleted, where a positive
                                                                                                                                                                                                                                                                                                                                                                                                                                       derangements of chromosome 9p21. Underlying the invention is the discovery that such derangements have their genesis in deletions occurring centromeric to STS 3.21, most often including breakpoints in exon 8 and/or between exons 4 and 5 of the gene which encodes MTAP. As the cancer and tumour development advance, deletions in 9p21 progress centromerically from the genesis point toward the gene encoding p16. Thus, the method of the invention is performed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 p15IINK4B (p15) with its alternatively spliced form p10, p16IINK4A (p16) and p19ARF, and the gene for methylthioadenosine phosphorylase (MTAP). The invention provides a method for diagnosis of, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the nucleotide sequence of a cosmid that includes sequences spanning human chromosome 9p21 (ATCC AC00047). This region harbours 5 genes within about 120 kb: the tumour suppressor genes p15IINK4B (p15) with its alternatively spliced form p10, p16IINK4A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 7; 55pp; English.
                                                                                                                                bladder cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           determining a prognosis for, cancer causatively associated
Local
     Similarity
                                                                                                                              or a chondrosarcoma (claimed).
27.6%; 58.1%;
  Score 28.4;
Pred. No. 3
                                DВ
                             21;
                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 With
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Š В Q 밁 5910 CACATAAAATCACTGTCTTTTCCAGG 5935 5850 TAAATTGAAAAAAGTTTAAATTAGTTATGTTTCTCCCCTGCAAACTTAAAAAAACACACA 5909 65 5 TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA 64 CAGTTAAAAAAACGGTATTTCCCTGG 90 Gaps

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RESULT 19
AAH08436
ID AAH08
AC XXX AC
                                                                                                                                                                                        27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human cDNA clone (5'-primer) SEQ ID NO:5271.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAH08436 standard; cDNA; 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                          (HELI-) HELIX RES INST
                                                                                                                                                                                                                                                                                                                                                29-JUL-1999;
                                                                                                                                        99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection; diagnosis; antisense therapy; gene therapy;
                                                                                                                                                                                                                                                                                                                                                99JP-0248036
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RESULT 20
AAA18260
ID AAA18
XX
AC AAA18
AC AAA18
DT 26-JI
XX
DT 26-JI
XX
Huma
XX
Huma
XX
Homc
XX
PD 07-
XX
PF 28-
XX
PR 29-
PR 11
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Best Local
 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
                                                                                                   07-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence and an oligonucleotide comprising a sequence, where the oligonucleotide which comprises a 3'-end sequence, where the oligonucleotide which comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primers sets can be used in antisense therapy and in gene therapy. The primers enc useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632 represent invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligonord primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end sequence complementary to the complementary strand of a polynucleotide which comprises a 5' end
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Ishii S,
                                                                                                                                   EP1074617-A2.
                                                                                                                                                                                                                                                                                                                              AAH18260 standard; cDNA; 2362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                  28-JUL-2000; 2000EP-0116126
                                                                                                                                                                                                   Human; primer;
                                                                                                                                                                                                                                Human cDNA sequence SEQ ID NO:18222.
                                                                                                                                                                                                                                                                    26-JUN-2001
                                                                                                                                                                                                                                                                                                    AAH18260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    424
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                                                                                                                                                                                                                                                                                                                                                                                                                                        AAAACGGTATTTC
                                                                                                                                                                                                                                                                                                                                                                                                                   AGAGACACCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACAACCTTTTAAGGATATCATTAACAACACATCCCTTGCGGAATTGGAAAAGCGGTTAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B₽;
     2000JP-0118776
                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                             detection; diagnosis; antisense therapy; gene therapy;
             99JP-0300253
                                   99JP-0248036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa T, Hayashi K, S
T, Wakamatsu A, Nagai K,
                                                                                                                                                                                                                                                                entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; 170
                                                                                                                                                                                                                                                                                                                                                                                                                   496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 28.2; D: Pred. No. 21; O: Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u>.</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises a polynucleotide which comprises 5'-end CC complementary strand of a polynucleotide which comprises 5'-end cC complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a CC polynucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 1-least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in CC the specification. The primers sets can be used in antisense therapy and CC in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13620 represent oligonucleotides, all of which are used in the exemplification of the present invention.
  Ota T,
Ishii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and/or diagnosis of the abnormality full-length cDNAs - \,
  Sequence 2362 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 8; SEQ ID 18222;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Primer sets for sy
full-length cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-MAY-2000; 2000JP-0183767
09-JUN-2000; 2000JP-0241899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-318749/34.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for synthesizing polynucleotides, particularly the cDNAs defined in the specification, and for the det nosis of the abnormality of the proteins encoded by
659 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nishikawa
T, Wakama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hikawa T,
Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2537pp + CD
  512
C;
562 G; 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English
  T;
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Otsuki
  other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamamoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         detection
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RESULT 21
AAZ43957
멍
      Key
                                            DAN; deadenylating nuclease; cytostatic; immunosuppressor; neuroprotector; anti-inflammatory; cancer; autoimmune disea
                                                                    Human
                                                                                   17-MAR-2000
                                                                                                    AAZ43957;
                                                                                                                   AAZ43957 standard;
                             Homo
                             sapiens
                                                                                                                                                          484 AGAGACACCTTTC
                                                                    DAN CDNA
                                                                                   (first
    Location/Qualifiers 58..1977
                                                                                                                   CDNA; 3002
                                                                                   entry)
                                                                                                                                                          496
                                                                                                                   ВP
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disease;

Qy

73

AAAACGGTATTTC

85

ACAACCTTTTAAGGATATCATTAACAACACCTTGCGGAATTGGAAAAGCGGTTAAA ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA

483 72 0

Б δÃ

Matches Query Match Best Local :

Similarity

27.4%; 61.6%;

Conservative

0

Pred. No. 25; 0; Mismatches Score 28.2; Pred. No. 25;

28; 22;

Gaps

DВ

Length Indels

2362; 0

T W 45;

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RRESULT 2:
ACC46483
ID ACC46484
XX ACC4
XX ACC4
XX ACC4
DT 02--1
XX Hume
XX Hume
XX Ganc
KW Canc
KW inff
KW inff
KW inf
KW gene
KW Goor
KW Goor
KW Goor
KW Oose
Home
XX Hume
XX Goor
XX Home
X
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Best Local
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                                                                                                                                                                                                                                                                                                                                            connective tissue disorder; drug screening; proteome analysis; gene therapy; antisense therapy; genotyping; transgenic animal; disease model; toxicological testing; transcript imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer; cell proliferative disorder; autoimmune disorder;
inflammatory disorder; infection; hormonal disorder; metabolic disorder;
neurological disorder; gastrointestinal disorder; transport disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Huels C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-NOV-1999
                                                                                                                                                                                                                                                                                                            nucleic acid synthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human dithp nucleic acid synthesis/modification protein-encoding cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC46483 standard; cDNA; 3073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3002 BP; 869 A; 633 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alzheimer's disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9958647-A2
                                                                                                                                    WO200297031-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         encoding a human deadenylation nuclease, used to,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73 AAAACGGTATTTC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGAGACACCTTTC 1122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACAACCTTTTAAGGATATCATTAACAACACCTTCCCTTGCGGAATTGGAAAAGCGGTTAAA 1109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Page 39-40; 46pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gallert K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98DE-1022122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27.48;
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                                                                                                                                                                                                                                                                                                            nucleic
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Pred. No. 27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28;
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                                                                                                                                                                                                                                                                                                                                                                                         knock in;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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B
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                                                                                                                                                    The invention relates to novel human diagnostic and therapeutic complynucleotides designated dithp (ACC46080-ACC46749) and to their compounds proteins (DITHP; ABR41136-ABR41812). The invention also relates to polynucleotide sequences at least 90% identical to the dithp cDNA compounds of the invention; recombinant vectors, host cells and compounds which specifically bind a DITHP proteins; microarrays comprising a dithp nucleic acid sequences; methods comproteins; microarrays comprising dithp nucleic acid sequences; methods of screening compounds which specifically bind a DITHP protein; and methods of screening compounds which specifically bind a DITHP protein and other cell grobe. Dithp nucleic acid sequences and DITHP protein may be used in the compounds which specifically bind a DITHP protein may be used in the compounds which specifically bind a DITHP protein may be used in the compounds using a dithp hybridisation comprobe. Dithp nucleic acid sequences and DITHP proteins may be used in the compounds using a dithp hybridisation comprobe. Dithp nucleic acid sequences and DITHP proteins may be used in the compounds using a dithp hybridisation comprobe. Dithp nucleic acid sequences; metabolic compounds using a dithp hybridisation comprobes and connective tissue disorders; hormonal disorders; metabolic considers; not protein activity or gene expression. DITHP compounds and connective tissue disorders. They may also be used to correct for modulators of protein activity or gene expression. DITHP corrections can additionally be used in analysis of the proteome of a tissue of corrections can additionally be used in analysis of the proteome of a tissue of corrections can additionally be used in analysis of the proteome of a tissue of corrections can additionally be used in analysis of the proteome of a tissue of corrections can additionally be used in analysis of the proteome of a tissue of corrections can additionally be used in analysis of the proteome of a tissue of corrections of the correction of individuals, in 
                                                                                           Query Match
Best Local
                                                                         Matches
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29-MAR-2001;
29-MAR-2001;
16-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel human diagnostic and therapeutic polypeptide useful for identifying test compound which specifically binds to a polypeptide encoded by human diagnostic and therapeutic polynucleotide, and to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19-JUN-2001;
20-JUN-2001;
                                                                                                                                                Sequence 3073 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; SEQ ID No 404; 591pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       induce antibodies
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P-PSDB; ABR41545.
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 1133 ACAACCTTTTAAGGATATCATTAACAACACCTTGCGGAATTGGAAAAGCGGTTAAA 1192
                                   13
                                                                                         Similarity
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                                   ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
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; 2001US-291280P.
; 2001US-291829P.
; 2001US-291849P.
; 2001US-299428P.
; 2001US-299776P.
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                                                                                                                                                    861 A;
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                                                                                         27.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yu JY, Tuason O,
Liu TF, Nguyen DA,
Lewis SA, Chen AJ,
                                                                                                                                                  662 C;
                                                                                           Score 28.2; DB
Pred. No. 27;
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                                                                       Mismatches
                                                                                                                                                    735 G;
                                                                                                                                                    815 T;
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O, Yap PE, Amshey SR;
DA, Kleefeld Y, Gerstin EH;
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73 AAAACGGTATTTC

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27-APR-2000;
20-JUN-2000;
                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 886-889; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding polypeptides with cytokine-like useful in diagnosis and gene therapy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                           activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and
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                                                                                                                                                                                                                                             Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
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DB; AAM78485.
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                                                                                                                         Similarity
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Wang D,
Yang Y,
ACAACCTTTTAAGGATATCATTAACAACACATCCCTTGCGGAATTGGAAAAGCGGTTAAA 1192
                                          ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA
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2000US-0528075
2000US-0620325
2000US-0654936
2000US-0663561
2000US-0693325
                                                                                                     Conservative
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Wejhrman T,
                                                                                                                                                                                             873 A; 664 C; 729 G; 812 T; 0 other;
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Wang J, Zhang J,
                                                                                                                    27.48; 61.68;
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                                                                                                                      Score 28.2;
Pred. No. 27;
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                                                                                                       encoded polypeptides (AAM78333-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of carear levieuring activity in the diagnosis and/or treatment of carear levieuring and may be useful in the diagnosis and/or treatment of carear levieuring and may be useful in the diagnosis and/or treatment of carear levieuring and may be useful in the diagnosis and/or treatment of carear levieuring activity and may be useful in the diagnosis and/or treatment of carear levieuring activity and may be useful in the diagnosis and/or treatment of carear levieuring activity and may be useful in the diagnosis and/or treatment of carear levieuring activity.
                             Note: Records for SEQ ID NO 2110 (AAK52581), (AAM80020) are omitted as the relevant pages were missing at the time of publication.
                                                                                                                                                                                                                                         The invention relates to polynucleotides (AAK51456-AAK53435) and the
                                                                                                                                                                                                                                                                      Claim 1; Page 4503-4504; 6221pp; English.
                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy -
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27-APR-2000;
                                                                                inflammation.
                                                                                             treatment of cancer, leukaemia, nervous system disorders,
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DB; AAM79469.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    system disorder; arthritis; inflammation;
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Yang Y,
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                                                                                                                                                                                                                                                                                                    diagnosis
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2000US-0560875
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Wejhrman
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immunomodulatory; cancer; leukaemia;
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, Zhang J, Ren
n T, Goodrich R;
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growth factor; haematopoiesis;
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| F, C
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Query Match Best Local Similarity

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Score 28.2; Pred. No. 27;

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Length Indels

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Sequence

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873 A; 668 27.4%; 61.6%;

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1 other;

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| 73 AAAAC 1170 AGAGA 7 25 978/c AAZ64978; 05-APR-2000 (Membrane-bound Membrane-bound Pharmaceutical HOMO Sapiens. WO9963088-A2. 09-DEC-1999. 02-JUN-1998. 02-JUN-1998. 02-JUN-1998. 04-JUN-1998. 05-JUN-1998. 10-JUN-1998. 10-JUN-1998. 10-JUN-1998. 10-JUN-1998. 10-JUN-1998. 10-JUN-1998. 11-JUN-1998. | 13 ATAAC 1110 ACAAC |
| GTATTTC 1182 | ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA |
| mapping; ss. | GTGAATTGCTAATACAGTTAAA 72 CGGAATTGGAAAAGCGGTTAAA 1169 |
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| 980S-0089948 980S-0089948 980S-0089948 980S-0099252 980S-0099429 980S-0099429 980S-0099445 980S-0099445 980S-0099445 980S-0099445 980S-0099654 980S-0099654 980S-0099664 980S-0099664 980S-0099664 980S-0099664 980S-0099666 | 805-008 800-808 |

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ARESULT 26
AAF44124/C
ID AAF44124 standard; c
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AAF44124;
AC AAF44124;
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DT 02-APR-2001 (first.)
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DE Human EST DNA16829 n
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24-AUG-1998;
26-AUG-1998;
  Human; secreted and
                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor impuncations are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baker K,
Wood WI,
                                                                                                                                                                                                                                                                                                                                                                      are useful as hybridization probes, in chrothe generation of antisense RNA and DNA. PR will also be useful for the preparation of
                                                                                                                                                                                                                                                                                                                                    Sequence 466 BP;
                                                                                                                                                                                                                                                                                                                                                           by recombinant techniques.
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                                                                                                                                                                                                                           TGAGTGGTTNAAATCTTTCATGGTGGGATAAATAACAGCTGCATCTATGATAATCCACCA
                                                                                                                                                                                                                                              TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA
                          DNA16829 nucleotide sequence SEQ ID NO:106.
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Yuan
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98US-0097971.
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                                                                                                        cDNA; 466
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 transmembrane protein;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                     in chromosome and gene mapping and in DNA. PRO nucleic acid sequences tion of PRO polypeptides, especially
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21;
PRO; cytostatic;
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08-OCT-1999;
30-NOV-1999;
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28-JUL-1999;
17-AUG-1999;
15-SEP-1999;
                                           02-MAR-2000;
15-MAR-2000;
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(GETH ) GENENTECH INC.
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07-JUL-1999;
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                          99WO-US21090.
99WO-US21547.
99US-0118663.
99WO-US28313.
99WO-US28313.
99WO-US28301.
99WO-US30095.
99WO-US30095.
2000WO-US00219.
2000WO-US00376.
2000WO-US04414.
2000WO-US04414.
2000WO-US04914.
2000WO-US04914.
2000WO-US06884.
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99US-0144758
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99US-0141037.
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ; Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF; Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI; Zhang Z;

WPI; 2001-032160/04

PRO polynucleotides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death -

Example 25; Fig 60; 935pp; English.

The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins can be used for targeted delivery of bloactive molecules, such as toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide sequences, and their fragments, can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. ARF44270 to ARF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AARF44269 and AARF41264 to AARF4300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.

Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;

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Query Match 27.2%; Score 28; DB 22; Length 466; Best Local Similarity 59.7%; Pred. No. 21; Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps
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 2000WO-US00219
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28-AUG-2001;
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07-MAY 1998
28-MAY 1998
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16-JUN-1998;
16-JUN-1998;
16-JUN-1998;
16-JUN-1998;
17-JUN-1998;
17-JUN-1998;
             Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
                                                                                                                   Roy MA,
Zhang Z;
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Ferrara N, Fong S, Gerber
Grimaldi JC, Gurney AL, Kl
Roy MA, Stewart TA, Tumas
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24-NOV-1997
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2000WO-US30952.
2000WO-US306520.
2001WO-US17800.
2001WO-US17800.
2001WO-US17692.
2001WO-US21735.
2001WO-US21735.
97US-049787.
97US-065186P.
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98US-088217P

98US-088655P

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98US-089908P
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                                                                                                                               KP, Botstein D, Desnoyers L, Eaton
Gerber H, Gerritsen ME, Goddard A,
AL, Kljavin IJ, Napier MA, Pan J,
Tumas D, Watanabe CK, Williams PM
                                                                                                                                                                                      Eaton
                                                                                                                                    Godowski PJ;
Paoni NF;
Wood WI;
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RESULT 28
ABX80693/c
ID ABX806
XX ABX806
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XX ABX806
XX ABX806
XX US ADX806
XX ADX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local :
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                                                                                                                                                                                                                                                          Human; gene; ss; PRO; secreted; transmembrane; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic; gene therapy; tumour-associated antigenic target; TAT; ADEPT;
        05-NOV-1997;
16-SEP-1998;
                                                                      15-NOV-2001; 2001US-0997428.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proliferation and/or redifferentiation of chondrocytes in culture are thus useful for treating sports injuries, and arthritis. This sequence represents a novel human PRO protein polynucleotide.
                                                                                                               06-FEB-2003
                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                      antibody-dependent enzyme
                                                                                                                                                                                                                                                                                                                                             Human secreted/transmembrane protein cDNA, #38.
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        97WO-US20069
98WO-US19330
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59.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              an isolated human PRO polypeptide. The PRO in detecting PRO polypeptides in a sample,
                                                                                                                                                                                                                                    mediated prodrug therapy; cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; 115 G; 149 T; 9 other;
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heart and is thus
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16 - JUN - 1997;
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2000WO-US30952.
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17-AUG-1998;
17-AUG-1998;
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17-AUG-1998;
17-AUG-1998;
18-AUG-1998;
                                                                                             Human; PRO; hypertrophy of neonatal heart; anglogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; addrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGET inhibition; endothelial cell growth inhibitor; T-lymphocytes stimulation; retinal neurons cell survival; rod photoreceptor cell survival; retinal disorder; retinitis pigmentosum; kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis; gene; ds.
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17-AUG-1998;
17-AUG-1998;
14-NOV-2001; 2001US-0990562.
                        06-FEB-2003
                                                US2003027985-A1
                                                                                                                                                                                                                                       Novel human secreted or transmembrane protein related DNA28357.
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98US-098014P.
98US-0980525P.
98US-100654P.
98US-113296P.
98US-13357P.
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RESULT 30
ABX90166/c
ID ABX90166;
XX
ABX90166;
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C ABX90166;
XX
DT 01-MAY-2003 (first entry)
XX
Human secreted/transmembrane pr
XX
Example of the secreted of transmembrane pr
XX

WW Human; gene; ss; PRO; secreted;
KW Human; gene; ss; PRO; secreted;
KW Human; gene; ss; PRO; secreted;
KW Human; gene; ss; PRO; secreted;
the secreted/transmembrane pr
XX

DE Homo sapiens.
XX
US2002160384-A1.
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PN US2002160384-A1.
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XX
PN 1-SEP-1998; 97WO-US20069.
PR 16-SEP-1998; 98WO-US210437.
PR 07-OCT-1998; 98WO-US21141.
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PR 01-DEC-1998; 98WO-US2118.
PR 01-DEC-1998; 99WO-US00106.
PR 05-JAN-1999; 99WO-US0252.
PR 05-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21090.
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17-AUG-1998;
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18-AUG-1998;
26-AUG-1998;
                                                                                                                                                                                                                                                                                                            Human secreted/transmembrane protein cDNA, #38
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nilarity 59.7%;
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98US-096758P

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Pred. No. 21;
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gene therapy.
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99WO-US28301.
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99WO-US30095.
99WO-US30911.
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The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bloactive combination of the properties and for modulating at least one biological activity of a cell. The PRO polypeptides or polypeptides or polypeptides are also useful in gene therapy, in chromosome dentification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein completides are useful as molecular markers for protein celectrophoresis, and the isolated nucleic acids may be used for electrophoresis, and the isolated nucleic acids may also be used in tissue typing. Anti-PRO antibodies are useful in diagnostic assays for PRO, and in affinity purification of PRO from recombinant cell culture or natural sources. The sequences presented in ARS90083-ABX90468 are the genes encoding, the primers amplifying and the probes detecting the PRO palypucleotides of the invention.

Note: The sequence data for this patent is also available in electronic format from USPTO at sequance.html.
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Matches 46
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                                                                                        Human PRO polynucleotide #163.
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     PRO; gene; ss; cytostatic; horse; cow; dog; cat; shee;
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Stewart TA,
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98US-089601P
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Gerber H, Gerritsen ME, Goddard A,
AL, Kljavin IJ, Napier MA, Pan J,
Tumas D, Watanabe CK, Williams PM,
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  tumour; cancer; breast; lung; stomach;
p; pig; goat; rabbit; ADEPT;
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99WO-US30095
99WO-US30095
2000WO-US002376
2000WO-US004914
2000WO-US044914
2000WO-US05044
2000WO-US05044
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99WO-US21547.
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10-JUN-1998; 10-JUN-1998; 10-JUN-1998;

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RESULT 32:
ABX79373/c
ID ABX79373 standard; C
XX
AC ABX79373;
XC ABX79373;
XX
DT 17-APR-2003 (first
XX
DF Human sectreted/tran
XX
KW Human; gene; ss; PRO
KW pharmaceutical; diag
KW colon cancer; lung c
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OS Homo sapiens.
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                                                              Human sectreted/transmembrane protein cDNA, #38.
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98US-095321P.
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24-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 24-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 25-JUN-1998 26-JUN-1998 26-JUN-1998 26-JUN-1998 26-JUN-1998 26-JUN-1998 26-JUL-1998 01-JUL-1998 02-JUL-1998 03-JUL-1998 04-AUG-1998 04-AUG-1998 04-AUG-1998

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11-FEB-2000

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30-NOV-1999
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2001WO-US21735
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98US-0888212P

98US-089914P

98US-089998P

98US-0899998P
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(GETH) GENENTECH INC.

Ashkenazi AJ, Ferrara N, Fo Grimaldi JC, Roy MA, Zhang Z; Stewart TA, J, Baker KP, Botstein D, Desnoyers L, Eaton Fong S, Gerber H, Gerritsen Me, Goddard A, Gurney AL, Kljavin IJ, Napier MA, Pan J, Gewart TA, Tumas D, Watanabe CK, Williams PM, Paoni DL; Godowski PJ; Paoni NF; Wood WI;

WPI; 2003-155950/15.

New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers

Example 25; Fig 60; 647pp; English.

The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful as pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes cance may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABX79290-ABX79675 are the genes encoding, the primers amplifying and the probes detecting the PRO polypucleotides of the invention.

Note: The sequence data for this patent is also available in electronic format from USPTO at seqdata.uspto.gov/sequence.html.

Sequence 466 BP; 116 A; 77 C; 115 G; 149 T; 9 other;

Matches Query Match Best Local 46; Similarity Conservative 27.2%; 0; Score Pred. core 28; DB red. No. 21; Mismatches 25; 31; Length 466; Indels 0; Gaps

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RESULT 33

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XX ABX640

XX ABX640

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XX Human;

KW Genet

XX Genet

XX US2002

XX US2002

XX US2002

XX US2002

XX O5-NON

PR 11-SEI

PR 01-DEC

PR 01-DEC

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PR 10-JAI

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PR 21-FE

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16-DEC-1990
11-FEB-2000
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15-MAR-2000
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11-MAC-2000
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16-SEP-1998;
17-SEP-1998;
07-OCT-1998;
01-DEC-1998;
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156 CCCTGTAAAAAATAGTA 140
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2000WO-USO34341.
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2000WO-USO5044.
2000WO-USO50841.
2000WO-USO5084.
2000WO-USO5084.
2000WO-USO53358.
2000WO-US13358.
2000WO-US14442.
2000WO-US14442.
2000WO-US14941.
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2001WO-US23756.
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99WO-US05028.
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98WO-US25108
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immunosuppressive; transgenic;
       13 NOV-1997
24 NOV-1997
25 FEB 1998
20 -MAR-1998
22 -APR-1998
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11 -JUN-1998
The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for linking bioactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO
                                                                                                                                                                                                                                                                                  Zhang
                                                                                                                                                                    Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers -
                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                   Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A,
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM,
                                                                                                                                 Disclosure; Fig
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97US-062250P.
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98US-089801P
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                                                                                                                               60; 649pp; English.
                                                                                                                                                                                                                                                                                                   Godowski
Paoni NF;
Wood WI;
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ΡJ

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RESULT 34
ABX16976/c
ID ABX169
XX ABX169
XX ABX169
XX Human;
KW Human;
KW Homo s
XX Ho
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Matches 46
           16-SEP-1998
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17-SEP-1998
07-OCT-1998
07-OCT-1999
05-JAN-1999
08-MAR-1999
08-MAR-1999
15-SEP-1999
15-SEP-1999
15-SEP-1999
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Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              05-SEP-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; PRO; gene; ss; secreted polypeptide; transmembrane polypeptide; toxin; radiolabel; ceil death; gene mapping; chromosome mapping; protein electrophoresis; genetic disorder; immunosuppressive; cytostat
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46; Conserv
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        99WO-US30911.
2000WO-US00219.
2000WO-US00376.
2000WO-US03565.
2000WO-US04341.
2000WO-US044414.
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99WO-US05028.
99WO-US12252.
99WO-US21254.
99WO-US21547.
99WO-US28313.
99WO-US28301.
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99WO-US30095
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     24-FEB-2000;
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02-MAR-2000;
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22-MAY-2000;
23-MAY-2000;
24-AUG-2000;
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28-AUG-2001;
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2000WO-US14042
2000WO-US22031
2000WO-US23528
2000WO-US23528
2000WO-US23528
2000WO-US23652
2000WO-US23652
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2001WO-US16652
2001WO-US16652
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2001WO-US16666
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2001WO-US21736
2001WO-US16667
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2001WO-US16662
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RESULT 35
ABS76828/c
ID ABS768
XX ABS768
XX 12-DEC
XX Frog e
XX Frog;
KW microa
XX Microa
XX Wenopu
XX Yenopu
XX Yenopu
XX 27-JUN
XX 23-JUL
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     markers. The polynucleotide is also useful as a hybridisation probe, in chromosome and gene mapping, in generation of antisense RNA and DNA, in the preparation of PRO polypeptide, for generating transgenic animals or knockout animals which in turn are useful in the development and screening of therapeutically useful reagents, to construct hybridisation probes for mapping the gene which encodes PRO and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as a chromosome marker and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. This sequence represents a human PRO polynucleotide of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Roy MA,
Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               molecule to a cell expressing the above polypeptides, where the bioactive molecule is a toxin, radiolabel or an antibody. The bioactive material causes the death of the cell. The polypeptide is useful for identifying agonists or antagonists of the PRO polypeptide, for preparing variants of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel secreted and transmembrane polypeptide for modulating activity of cell expressing the polypeptide, identifying againtagonists of polypeptide, and as molecular weight markers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Ferrara N, Fong S, Gerber H, Gerritsen ME, Godd Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Roy MA, Stewart TA, Tumas D, Watanabe CK, Willi
                                                                                                                             Frog; ss; embryonic development; developmental disorder;
microarray; cell differentiation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRO, as a molecular weight marker for protein electrophoresis purposes and the PRO polynucleotide is useful for recombinantly expressing those
                                                                 US2002081610-A1
                                                                                                                                                                         Frog embryonic gene sequence Q9925237 #1
                                                                                                                                                                                                            12-DEC-2002
                                                                                                                                                                                                                                           ABS76828
                                                                                                                                                                                                                                                                         ABS76828 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 60; 655pp; English
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 23-JUL-2001; 2001US-0910943.
                                  27-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                     156
                                                                                                                                                                                                                                                                                                                                                                                                                   216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             27.2%;
1 Similarity 59.7%;
46; Conservation
                                                                                                                                                                                                                                                                                                                                                                                  65 CAGTTAAAAAAACGGTA 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ഗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for detecting PRO polypeptides and for linking a bioactive to a cell expressing the above polypeptides, where the
                                                                                                                                                                                                                                                                                                                                                     CCCTGTAAAAAATAGTA 140
                                                                                                                                                                                                                                                                                                                                                                                                                  TGAGTGGTTNAAATCTTTCATGGTGGGATAAATAACAGCTGCATCTATGATAATCCACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                               TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             466 BP; 116
                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lates to a secreted and transmembrane polypeptide, and the polynucleotide encoding it. The polypepti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KP, Botstein D,
Gerber H, Gerri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; 77 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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Pred. No. 21;
                                                                                                                                                                                                                                                                         ΒP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
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C MA, Pan J,
Williams PM,
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MA, Pan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 466
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                                                                                                                                                                                                                                                                                                                                                                                                                  157
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ABS76832/c
ID. ABS76832 standard; cDNA;
   В
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Best Local
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Frog

embryonic gene sequence Q9925237

12-DEC-2002 ABS76832;

(first

entry)

725

ВP

604

TTGACCAATGGATATTGCTTTCTT 581 TAAAAAAACGGTATTTCCCTGGTT 92

69

49; 9

Conservative

0,

Mismatches

0

Gaps

0

Similarity

27.2%; 58.3%;

Score 28; Pred. No.

23; 24; 35;

Length Indels

664 TGTCATTTCTTTTAACTGGCAATTGTAATATCTTGTGTTTTCTGTGTTTTTGCGATTACAGT

605 89

TGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGT

Frog; ss; embryonic development; developmental disorder; microarray; cell differentiation.

21-JUL-2000; 2000US-219658P 23-JUL-2001; 2001US-0910943. 27 - JUN - 2002 US2002081610-A1 Xenopus laevis

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20 contiguous nucleotides of one of those sequences. Also included are detecting differential expression of embryonic genes, comprising:
(a) contacting a nucleic acid array comprising genes expressed in embryonic but not mature cells with nucleic acids from sample and control cells; and (b) detecting differential hybridisation of nucleic acids from the sample cells relative to the control cells; and detecting defects in development, comprising: (a) contacting nucleic acids from the sample cells relative to the control cells; and detecting defects in development, comprising: (a) contacting nucleic acids from test cells undergoing development with a nucleic acid array of gene products known to play a fundamental role in the development process; and (b) detecting a difference in expression of a fundamental gene in the sample cells relative to a standard. The invention is useful to identify
                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to a nucleic acid array, where each coordinate contains a single nucleic acid species having one of 770 nucleotide sequences (appearing as ABS/6747-ABS/7516) a of a Xenopus embryonic product, or its complement or hybridisable fragment of not less than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid array containing Xenopus embryonic nucleic acids is useful to identify genes involved in embryonic development, to identify different types of embryonic cells, and to diagnose developmental
                                                genes involved in embryonic development and related processes such as cell differentiation. This would be useful for diagnosing developmental disorders and for identifying different types of embryonic cells. The present sequence is one of the 770 Xenopus embryonic cDNA sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 98; 823pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-626534/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-JUL-2000; 2000US-219658P
Sequence 725
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hemmati-Brivanlou A, Altmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYRQ ) UNIV ROCKEFELLER
  B₽;
215 A; 137 C; 165 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CR;
206 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene
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The invention relates to a nucleic acid array, where each coordinate contains a single nucleic acid species having one of 770 nucleotide Sequences (appearing as ABS77516) a of a Xenopus embryonic gene CC product, or its complement or hybridisable fragment of not less than C20 contiguous nucleotides of one of those sequences. Also included are CC detecting differential expression of embryonic genes, comprising: CC (a) contacting a nucleic acid array comprising genes expressed in CC embryonic but not mature cells with nucleic acids from sample and CC control cells; and (b) detecting differential hybridisation of nucleic acids from the sample cells relative to the control cells; and detecting defects in development, comprising: (a) contacting nucleic acids from CC defects in development, comprising: (a) contacting nucleic acids from CC test cells undergoing development with a nucleic acid array of gene products known to play a fundamental role in the development process; and CC sample cells relative to a standard. The invention is useful to identify genes involved in embryonic development and related processes such as cell differentiation. This would be useful for diagnosing developmental CC disorders and for identifying different types of embryonic cells.
                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local s
Matches 49
  31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
                                                                                                                                                      Human; 1mmune; haematopoietic; immune/haematopoietic antigen; cancer;
                                                                                                                                                                                Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:8769
                                                  17-JAN-2001;
                                                                          09-AUG-2001
                                                                                                  WO200157182-A2
                                                                                                                                                cytostatic; gene
                                                                                                                                                                                                            06-NOV-2001
                                                                                                                                                                                                                                                            AAK63709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 725 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid array containing Xenopus embryonic nucleic acids is to identify genes involved in embryonic development, to identify different types of embryonic cells, and to diagnose developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is one of the 770 Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
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                                                                                                                         sapiens.
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                                                                                                                                                                                                                                                            standard;
                                                                                                                                                                                                                                                                                                                                                                   TGTCATTTCTTTTAACTGGCAATTGTAATATCTTGTGTTTTCTGTGTTTTTGCGATTACAGT
                                                                                                                                                                                                                                                                                                                                                                                       TGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGT
                                                                                                                                                                                                                                                                                                                     TTGACCAATGGATATTGCTTTCTT 581
                                                                                                                                                                                                                                                                                                                                             TAAAAAACGGTATTTCCCTGGTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page
  ; 2000US-0179065.
; 2000US-0180628.
; 2000US-0184664.
                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                           (first entry)
                                                  2001WO-US01354.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                215 A; 137 C; 165 G;
                                                                                                                                               therapy; vaccine; metastasis;
                                                                                                                                                                                                                                                            CDNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                              27.2%;
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                                                                                                                                                                                                                                                           378
                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                               Score 28; DB Pred. No. 23; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                206 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 725;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA sequences
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
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01-SEP-2000;
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01-SEP-2000;
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05-SEP-2000;
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06-SEP-2000;
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26-SEP-2000;
27-SEP-2000;
27-SEP-2000;
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08-SEP-2000;
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16-MAR-2000;
17-MAR-2000;
17-MAR-2000;
18-APR-2000;
19-MAY-2000;
07-JUN-2000;
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25-SEP-2000;
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21-SEP-2000;
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12-SEP-2000;
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30-JUN-2000;
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       2000US-0235834
2000US-0235836
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2000US-0237037
2000US-0237037
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2000US-0231968
2000US-0232397
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2000US-0232401
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2000US-0233064
2000US-0233064
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2000US-0234223
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2000US-0231242.
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2000US-0225759.
2000US-0226279.
2000US-0226681.
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2000US-0227182.
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2000US-0225266
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2000US-0215135.

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2000US-0189874.
2000US-0190076.
2000US-0198123.
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17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
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05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
08-DEC-2000;
08-DEC-2000;
08-DEC-2000;
                                 Nucleic acids encoding useful for preventing, metastasis -
Claim 1; SEQ ID NO 8769; 3071pp + Sequence Listing; English
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                                                                                                                         2001-483426/52.
                                                                                                                                                         CA,
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                                                                                                                                                                                         HUMAN GENOME
                                                                                                                                                       Barash SC,
                                                                                                                                                                                                                           2001us-0259678
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2000US-0251869.
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2000US-0241787.
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                                                                                                                                                                                                                                                                                -0251989
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                                                                                                                                                                                         SCI INC
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                                                 human immune/hematopoietic antigen diagnosing and/or treating cancers
                                                   polypeptides,
and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC81718/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnose and treat immune/haematopoietic related diseases, especially cancers and cancer metastases of haematopoietic derived cells. ARK64703 to AAK8644 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK94942 to AAK84950 and AAM82169
                                                                                                                                                                                                                                                                                                                                                                                                                 antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antifungal; antiparasitic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disord neurological disease; infection; human; secreted protein; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC81718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC81718 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 378 BP; 125 A; 60 C; 71 G; 117 T; 5 other;
                                                                                                                                                                                                                         09-APR-1999; 99US-0128697
20-JAN-2000; 2000US-0176929
                                                                                                                                                                                                                                                                           06-APR-2000; 2000WO-US09067
                                                                                                                                                                                                                                                                                                               19-OCT-2000
                                                                                                                                                                                                                                                                                                                                                WO200061627-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human secreted protein coding sequence SEQ ID NO: 19
                                                                                 WPI; 2000-647419/62.
P-PSDB; AAB45394.
                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               represent sequences used in the exemplification of the present invention
                                                                                                                                     Rosen CA,
                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
(ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTATTTCCCTGGTTCTGATCCAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTGTTTTCATTRTAAGGAACAAA 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCTTAACARGATTAATAAATCACCCCAGTCTTAATTTTAAAAGACTTTTAAAATAT
                                                                                                                                     Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27.0%;
56.6%;
                                                                                                                                     Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
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Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                     disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68
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used

diagnosing,

New nucleic acid molecules encoding 49 human secreted proteins for diagnosing, preventing, treating or ameliorating medical conditions and used as food additives or preservatives -

nosing, preventing, treating or ame as food additives or preservatives

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RESULT 39
AAF86585/c
ID AAF86
XX AAF86
XX AAF86
XX AAP86
XX Sphin
XX Sphin
XX Sphin
XX Sphin
XX ICAC
XX ICAC
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer, and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to the isolation of genes AAC81710-C81758 encoding 49 human secreted proteins AAB45386-B54534. The genes can be used to generate fusion proteins by linking to the gene for the human immunoglobulin G Fc portion (SEQIDI) for increasing the stability of the fusion protein as compared to the human protein only. The genes and proteins are useful for preventing, ameliorating or treating medical conditions, e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The
Alpha-1,3-multi-branch dextran hydrolase gene, preparation of alpha-1,3-multi-branch dextran !
                                                                                               P-PSDB; AAB82125
                                                                                                                                                                                                                                                                                                      16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                       JP2001054382-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sphingobacterium sp. V-54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Alpha-1,3-multi-branch dextran hydrolase; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alpha-1,3-multi-branch dextran hydrolase gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAF86585
                                                                                                                                                                                 (NODA ) ZH NODA SANGYO KAGAKU KENKYUSHO
                                                                                                                                                                                                                                               16-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                             27-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF86585 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2024 BP; 649 A; 360 C; 319
                                                                                                                       2001-294617/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAAACGGTATTTCCCTGGTTCTGATCCAAC 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAAGATATTGATCTGACTGAAATATAAC 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATAAGAAGCTTACTATATCATTATTATAAGTAGCATATATTACTTTCAAATACCTATATT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                               99JP-0229541.
                                                                                                                                                                                                                                                                                                      99JP-0229541.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "Alpha-1,3-multi-branch
/partial
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26.8%;
56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 27.6;
Pred. No. 38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 694 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39;
   , for the recombinant hydrolase -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dextran hydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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RESULT 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                    The invention relates to human polynucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA0I3910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopolesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or restricts.
                                                                                                                                                                                                       Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukaemia, inflammation and immun
                                                                                                                                                                                                                                                WPI; 2001-514838/56
P-PSDB; AAO08975.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence was de can be used for the dextran hydrolase.
                                                                                                                                                                Claim 1; SEQ ID NO 8966; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                               28-FEB-2000;
18-MAY-2000;
             treatment of cancer, leukaemia, nervous system disorders, arthritis and
                                                                                                                                                                                                                                                                                                                    (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-2001; 2001WO-US04927
                                                                                                                                                                                                                                                                                                                                                                                                                     07-SEP-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200164835-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAI88906;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAI88906 standard; cDNA; 2552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human polynucleotide SEQ ID NO 8966
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example
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                                                                                                                                                                                                                                                                                           YT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2029 CAGCATAAATAGTTGCCAAATAGGTCATTCCTTCATCCAGAAAATCAAATTTTATCTTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1969 ATGTTCTGCTGGAA 1956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGTTCTGATCCAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2166 BP;
                                                                                                                                                                                                                                                                                          Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 9; 10pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence is alpha-1,3-multi-branch dextran hydrolase genece was derived from Sphingobacterium sp. V-54. This sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                               2000US-0515126
2000US-0577409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                           Drmanac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                721 A; 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinant preparation of alpha-1,3-multi-branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 27.6; D
Pred. No. 39;
0; Mismatches
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Best Local
        (esp. inability to process trypsinogen to trypsin). For cleaving fusion proteins, recombinant EK catalytic domain is much more efficient than the native two-chain holoenzyme and is not
                                                                                                              New nucleic acid encoding enterokinase activity vectors, host cells, expression products and antibuseful in treating digestive disorders and for che
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enterokinase; EK; heavy chain; light digestive disorder; cleavage; fusion trypsin; enzyme; PACE gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                     misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine enterokinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ70104 standard; cDNA;
contaminated by other proteolytic enzymes.
                                                       The enterokinase (EK) (or the EK gene when used in gene therapy)
                                                                                                                                                                                               Lavallie
                                                                                                                                                                                                                    (GEMY)
                                                                                                                                                                                                                                           15-JAN-1993;
                                                                                                                                                                                                                                                                 13-JAN-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ftp.wipo.int/pub/published_pct_sequences
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                                          to treat digestive disorders associated with low EK activity
                                                                                                                                                            1994-249229/30
DB; AAR57283.
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(first entry)
                                                                              26-27;
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/*tag= b
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/note= "C-terminal portion of heavy
/note= (non-catalytic domain)"
                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
1..1690
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                                                                                                                                                                                                                                                                                                                                  /note= "light chain (catalytic domain)"
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56.7%;
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                                                                              English.
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Pred. No. 40;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   light chain; catalytic domain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                               nd antibodies for cleaving
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β 29

ATAAGAAGCTTACTATATCATTATTAAGTAGCATATATTACTTTCAAATACCTATATT 2315

ATANCAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA

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RESULT 42
ABS70481
ID ABS70
AC ABS70
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Query Match
Best Local S
Matches 51
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Matches
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                                                                                                                                                                 The invention relates to a combination comprising a number of substantially purified and isolated polynucleotides which are co-expressed with genes known to be involved in bone remodelling are osteoporosis. The invention is used to diagnose disorders associate with bone remodelling or osteoporosis. ABS70344-ABS70512 represent
                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                         Claim 1; Column 343-346; 206pp; English.
                                                                                                                                                                                                                                                                                                                                                                       A combination of polynucleotides which are co-expressed with genes
known to be involved in bone remodeling and osteoporosis are useful
an array for the diagnosis of bone remodeling and osteoporosis
associated disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-673014/72.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-JAN-2000; 2000US-0484970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JAN-2000; 2000US-0484970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human bone remodelling gene #138.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27 - NOV - 2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABS70481;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                               human bone remodelling genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (Updated on 25-MAR-2003 to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ΚĄ,
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  51;
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                       Similarity
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                                                                                                 3054 BP;
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  Conservative
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                                                                                                 899 A; 643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         797 A; 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               osteoporosis; human;
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                       26.8%;
56.7%;
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                       Score 27.6;
Pred. No. 41;
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Pred. No. 40
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                                                                                                 620 G; 892 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           575 G;
  Mismatches
                                                                                                                                                  the invention
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  39;
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                                                Length
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Gaps
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RESULT 43
ABV47128
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AC ABV47
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                                                                                                                    Query Match
Best Local S
Matches 52
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                    Sequence 444

    (e) selecting a composition for inhibiting prostate cancer in a patient;
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                        (d) assessing the efficacy of a therapy for inhibiting
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (MILL-) MILLENNIUM PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-FEB-2001; 2001WO-US05171
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RESULT 44
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  Antibacterial;
                            N. gonorrhoeae
                                                        07-MAR-2003
                                                                                   ABZ41770;
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medicament f
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                                                                                                                                                                                                                            Sequence 588 BP; 186 A; 112 C; 122 G; 168 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     New protein from Neisseria gonorrheae, useful for the manufacture of a medicament for treating or preventing N. gonorrheae infection -
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P-PSDB; ABP80800.
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SUMMARIES

| AUTHORS TITLE JOURNAL | SOURCE ORGANISM | ACCESSION VERSION KEYWORDS | RESULT 1 AX119931 LOCUS DEFINITION | | Α. | C 43 | . 4 | - 4- | ωι | ພ ພ | ωı | C 34 | ωί | C 31 | ωĸ | 0 0 28 | N | c 25 | N | NN | N | c 19 | н і | | 15 | ۔ ۔ | c 12 | <u> </u> | | œ ~ | | | ο ດ • ω | 2 - | | Result No. | |
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| | a; Vertebrata; Euteleostomi; iini; Hominidae; Homo. | | A linear PAT 11-MAY-2001 | | 24223 Rattus n | Continuation (2 of | Sequence | Danio r | Homo sap | HOMO S | Homo sap | Homo sap | Homo sap | 7 Homo sa 7 Danio r | AC090142 Homo sapi | Homo sa | Rattus | w 01 | Rattus | Ra | 12 52091 | w C | Mus | ی س | 52 Mus mu | ALI39317 Human Chr AC097744 Rattus no | Sequer | · · | Rattus n | BV018667 S212P6240 | 57 Mus mus | AX119933 Sequence | 5 Human | | | Description | |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6543
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AATACAGTTAAAAAAACGGTATTTCCCTGGTT 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      69;
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (08-OCT-1999) Genome Centre, 1650 Cedar Ave., Montreal, QC H3G 1A4, Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF193556 12793 bp
Homo sapiens sacsin (SACS) gene,
AF193556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Richter, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bouchard, J.P., Mathieu, J., Melancon, S.B., Schallin
Lander, E.S., Morgan, K., Hudson, T.J. and Richter, A.
ARSACS, a spastic ataxia common in northeastern Qu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 12793)
Engert, J.C., Berube, P., Mercier, J., Dore, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Engert,J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AF193556.1 GI:6907041
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutations in a new gene encoding an 11.5-kb ORF t. Genet. 24 (2), 120-125 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to
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                                                /translation="mntfwpgrelivqwypfdenrnhpsvswlkmywknlyihfsedl
TLfDemPLIPRTILEEGQTCVELIRLRIPSLVILDDESEAQLPEFLADIVQKLGGFVL
KKLDASIQHFLIKKYIHSPLPSAVLQIMEKMFLQKLCNQITSLLPTHKDALRKFLASL
NPNVLEWLTPLKFIQISQEQMVSAGELFDPDIEVLKDLFCNEEGTYFPPSVFTSPDIL
                 SSDEATIRLANMLKIEQLKTTSCLKLVLKDIENAFYSHEEVTQLMLWVLENLSSLKNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9606"
2256 c 2487 g 388
                                   TDSSEKEKRIIQELAIFKRINHSSDQGISSYTKLKGCKVLHHTAKLPADLRLSISVID
                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
                                                                                                       /protein_id="AAF31262.1"
/db_xref="GI:6907042"
                                                                                                                                       'product="sacsin"
                                                                                                                                                          /codon_start=1
                                                                                                                                                                         'note="molecular chaperone"
                                                                                                                                                                                          /gene="SACS"
                                                                                                                                                                                                                           'product="sacsin"
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                                                                                                                                                                                                                                                                                                                map.
                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
/chromosome="13"
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/mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Berube, P., Dore, C., Lepage, P., Ge, B., Hudson, T.J. and
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75.0%;
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 12793;
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61

AATACAGTTAAAAAAACGGTATTTCCCTGGTT

92

6543 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTTGAATTTGC 6602

GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT

ORIGIN BASE COUNT

Query Match Best Local Matches

69;

Conservative

0, Score Pred.

Mismatches 55.2; No. 2

DB 9; 2.4e-05; nes 23;

Length 12793; Indels

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Gaps

60 0; Similarity

53.6%; 75.0%;

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4163
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ACIIIKLENFMQQKV"
2256 c 2487
                                                                                                                                                           KYSFORFYTSWNQEATSHKSERQQQNKEKCPPSAGQTYSQRFFVPPTFKSVGNPVEAR
RWLRQARANFSAARNDLHKNANEWVCFKCYLSTKLALIAADYAVRGKSDKDVKPTALA
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NQPFTEDDVRGIQNLGKGTKEGNPYKTGQYGIGFNSVYHITDCPSFISGNDILCIFDP
HARYAPGATSISPGRWFRDLDADFRTQFSDVLDLYLGTHFKLDNCTMFRFPLRNAEMA
                                                                                                             QKIEEYSQQLEGLTNDVHTLEAYGVDSLKTRYPDLLPFPQIPNDRFTSEVAMRVMECT
                                                                                                                                                                                                                                                                                                                                        SIPPLFSGRESHKTSSKHQSPKKLKVNSLPEILKEVTSVVEQAWKLPESERKKIIRRL
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KILKSLPCYKSISGRYVSIGKFGTCYVLTKSIPSAEVEKMTQSSSSAFLEEKIHLKEL
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CTKWKDNFASESWLKNAWHFISESVSVKEDQEETKPTFDIVVDTLKDWALLPGTKFTV
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ENFQLCRRIISEGIWSLIREKKQEFCEKNYGKILLPDTNLMLLPAKSLCYNDCPWIKV
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                                                                                                                                                                                                                                                                        YLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQSD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {	t ETPKVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALR}
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVINLEYESDFKPYLYKLPLELGTFHQLFKHLGTEDIISTKQYVEVLSRIFKNSEGKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DVLQLLWTSCPILPEKATPLSIKEQEGSDLGPQEQLEQVLNMLNVNLDPPLDKVINNC
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RRLGLVPCGAVGVQLSEIQDQKWTVKPHIGEVFCYLPLRIKTGLPVHINGCFAVTSNR
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QSSEGKMTLKKIKWVPACKERPPNYPGSLVWKGDLCNLCAPPDMCDVGHAILIGSSLP
                                                                                                                                                                                                                                                                                                                                                                                      NSSFLGKIYQIDIGYSEYKIYSSLDLYKFSRPEESSQSRDSAPSTPTSPTEFLTPGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LESLLIIHDANSRLKQAKHFYDRTVRVFEVMLPEKLFIPNDFFKKLEQLIKPKNHVTF
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RESULT 3
AL157766/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers giver in the feature table with their source databases: Em:, EMBL; Sw:,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requests: clonerequest@sanger.ac.uk
On Apr 12, 2001 this sequence version replaced g1:12709868.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92693 bp DNA linear PR Human DNA sequence from clone RP11-40020 on chromosome 13q12.11-12.2, complete sequence
                                                                                                                                                                                                                                                                                                                                                                                                       IMPORTANT: This sequence is not the entire insert of clone RP11-40020 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-750MI is at 92594 in this sequence right end of clone RP11-72P19 is at 100 in this sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RPI1-40020 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 13, constructed by the Sanger Centre Chromosome 13 mapping Group. Further information can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISSPROT; {\tt Tr:}, {\tt TREMBL}; {\tt Wp:}, {\tt WORMPEP}; {\tt Information} on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (11-APR-2001) Sanger Centre, Hinxton, Cambridgeshire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding to the overlapping clone, as we submit sequences with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tromans, A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 umalia; Eutheria; I
(bases 1 to 92693)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     //www.sanger.ac.uk/HGP/Chr13
                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UK. E-mail enquiries: humquery@sanger.ac.uk Clone
  /note="AluY repeat: matches 1.
                                                                                                                                                                     /note="MIR repeat: matches
                                                                                                                                                                                                                 'clone_lib="RPCI-11.1"
                                                                                                                                                                                                                                        /clone="RP11-40020"
                                                                                                                                                                                                                                                                             'chromosome="13"
                                         note="MER46C repeat: matches 1. .286 of consensus"
                                                                                                                                                      2673
                                                                                   Aluy repeat: matches 3.
                                                                                                                                                                                                                                                         11-12.2"
                                                                                                                             repeat: matches 68.
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  .310 of consensus
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/note="MER46A repeat: matches 1.
20613. .20912
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46754. .47052
                                                                                                       note="L1MB6"
                                                                                                                                             'note="AluSx repeat: matches
                                                                                                                                                                                                               'note="CpG island"
                                                                                                                                                                                                                                                       'note="AluSc repeat:
                                                                                                                                                                                                                                                                                             note="L2 repeat: matches 1685.
                                                                                                                                                                                                                                                                                                                                           'note="Alu
                                                                                                                                                                                                                                                                                                                                                                                                                        'note="L1MA10 repeat: matches 5950. .6322 of consensus"
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restriction digest data."
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/note="AluSg1 repeat: matches 1.
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                                                                                                                                                                                     evidence=not_experimental
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                                AATACAGTTAAAAAAACGGTATTTCCCTGGTT 92
                                                              GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTTGAATTGC
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62008. .63
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/note="MER31-internal repeat: matches
consensus"
72873. .73249
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71279. .71413
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62566. .62865
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                                                                                                                                                                                                                                                                             /note="MER31-internal repeat: matches 42. .175 of
                                                                                                                                                                                                                                                                                                               /note="AluSx repeat: matches 1. .295 of consensus"
                                                                                                                                                                                                                                                                                                                                            note="MER31A repeat: matches 47.
                                                                                                                                                                                                                                                                                                                                                                            /note="MER21B repeat: matches 548. .680 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                              70957.
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="MIR repeat:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           55571. .65640
/note="L1PB2 repeat: matches 5728. .5791 of consensus"
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55396. .65569
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                                                                                                                                0;
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                                                                                                                             Score 55.2; DB 9;
Pred. No. 1.9e-05;
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Genome Center

Center: Washington University Genome Sequencing
Web site:http://genome.wustl.edu/gsc/index.shtml

Project Information
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Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 99819) Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC079761 99819 bp
Homo sapiens chromosome UNK clone
PROGRESS ***, 44 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (10-SEP-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The sequence of Homo sapiens Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                   arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                               as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                    NOTE: This is a 'working draft' sequence. It currently consists of 44 contigs. The true order of the pieces is not known and their order in this sequence record is
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/db_xref="taxon:9606"
/chromosome="UNK"
                    /note="assembly_name:Contig40"
8671. .9925
                                         6858.
                                              /note="assembly_name:Contig39"
sasa os70
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 /note="assembly_name:Contig41"
10026. .11426
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                                                           ="assembly_name:Contig35"
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61105...64185
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48770. 50798
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11527. .13266
/note="assembly_name:Contig44"
13367. .14794
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35386. .37184
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25971. .27230
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'note="assembly_name:Contig47"
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Sequence 3
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AX119933.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sçiurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                    Submitted (08-OCT-1999) Genome Centre, Montreal General Hospital, 1650 Cedar Ave., Montreal, QC H3G 1A4, Canada
                                                                                                                                                                                                                                      Richter, A.
                                                                                                                                                                                                                                                    Engert, J.C.,
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                                                                                                                                                                                                                                                                                                                   SACS, a spastic ataxia common in northeastern Quebec, is caused mutations in a new gene encoding an 11.5-kb ORF t. Genet. 24 (2), 120-125 (2000)
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                                                                                                                                                                       Cedar Ave., Montreal, QC H3G
Location/Qualifiers
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3 from Patent WO0129266.
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
2280 c 2387 g 322
/protein_id="AAF31263.1"
                'product="sacsin"
                           /codon_start=]
                                            'note="molecular chaperone"
                                                                           product="sacsin"
                                                                                                          /db_xref="taxon:10090"
                                                                                                                            /mol_type="genomic
                                                                                                                                          /organism="Mus musculus"
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73.9%;
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red. No. 6.9e-05;
Mismatches 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                               Ge, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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BASE COUNT ORIGIN

3599

Query Match Best Local Similarity

52.0%; 73.9%;

Score Pred.

53.6; DB 10; No. 6.9e-05;

Length 11493;

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PIPAEIHYTLLMDPMNVFYPGEYVGYLVDAEGGDIYGSYQPTYTYAIIVQEVEREDAD
NTSFLGKIYQIDIGYSEYKIVSSLDLYKFSRPDESSQNRDSAPTTPTSPTEFLTPGLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LLSCHTANIDSPASILKAVHYMVQTSTFRTEKLMENDFEALLMYFNCNLSHLMSQDDI
KILKSLPCYKSISGRYMSIAKFGTCYVLTKSIPSAEVEKWTQSSSSAFLEEKVHLKEL
YEVLGCVPVDDLEVYLKHLLPKIENLSYDAKLEHLIYLKNRLASIEEPSEIKEQLFEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNGHFALDSARRNLWRDDNGVGVRSDWNNSLMTALIAPAYVELLIQLKKRYFPGSDPT
LSVLQNTPIHVVKDTLKKFLSFFPVNRLDLQPDLYCLVKALYSCIHEDMKRLLPVVRA
PNIDGSDLHSAVIITWINMSTSNKTRPFFDNLLQDELQHLKNADYNITTRKTVAENVY
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NQPFTEDDVRGIQNLGKGTKEGNPCKTGHYGIGFNSVYHITDCPSFISGNDILGIFDP
HARYAPGATSVSPGRWFRDLDADFRTQFSDVLDLYLGNHFKLDNCTMFRFPLRNAEMA
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ENFQLCRRIISEGIWSLIREKRQEFCEKNYGKILLPDTNLLLLLPAKSLCYNDCPWIKV
KDSTVKYCHADIPREVAVKLGAIPKRHKALERYASNICFTALGTEFGQKEKLTSRIKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ILLSLIDEKLKIKDPRAKDFAAKYQTIPFLPFLTKPAGFSLEWKGNSFKPETMFAATD
IYTAEYQDIVCLLQPILNENSHSFRGCGSVSLAVKEFLGLLKKPTVDLVINQLKQVAK
SVDDGITLYQENITNACYKYLHEAVLQNEMAKATIIEKLKPFCFILVENVYVESEKVS
                                                            SIPPLFSGKESHKSPSTKHHSPRKLKVNALPEILKEVTSVVEQAWKLPESERKKIIRR
                                                                                                                                                                                                                                                                                                                                                APHYKSRIQGNIGVQMLVDLSQCYLGKDHGFHTKLIMLFPQKLRPRLLSSILEEQLDE
ETPKVCQFGALCSLQGRLQLLLSSEQFITGLIRIMKHENDNAFLANEEKAIRLCKALR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MDLLSGNFLKELSLIPFLCPERAPAEYIRFHPQYQEVNGTLPLIKFNGAQVNPKFKQC
DVLQLLWTSCPILPEKATPLSIKEQEGSDLAPQEQLEQVLNMLNVNLDPPLDKVINNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GKLPCRLQQTNLKLFHSLKLLVDYCFKDAEESEFEVEGLPLLITLDSVLQIFDGKRPK
FLTTYHELIPSRKDLFMNTLYLKYSSVLLNCKVAKVFDISSFADLLSSVLPREYKTKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GFSSMEKVSKSVISAHKNQDITLFPRGGVAACITHNYKKPHRAFCFLPLSLETGLPFH
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GRFPYGSTQDYLNPIILIKLVQLGMAKDDILMDDMLERAESVAEINKSDHAAACLRSS
LYLKWHPDKNPENHDIANEVFKHLQNEINRLEKQAFLDQNADRASRRTFSTSASRFQS
                                                                                                                                                                                                                                    ALAMTLKSATDNLISDTSYLIAMLGCNDIYRISEKLDSLGVKYDSSEPSKLELPMPGT
                                                                                                                                                                                                                                                                                    EGLKVSCFEKLQTTLRVKGFNPIPHSRSETFAFLKRFGNAVILLYIQHSDSKDINFLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVINLEYEADFKPYLYKLPLELGTFHQLFKHLGTEDIISTKQYVEVLSRIFKSSEGKQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RNICNITTLDEEMVKTRAKVLRSIYEFLSAEKREFRFQLRGVAFVMVEDGWKLLKPEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {	t MTSWVEFLRNIGLKYALSQQQLLQFAKEISVRANTENWSKETLQSTVDILLHHIFQER}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STSQLVVPEGDVLIPLSLMHIAVFPNAQSDKVFHALMKAGCIQLALNKICSKDSALVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        {\tt CAKWKDNFASESWLKNAWHFISESVSVTDDQEEPKPAFDVIVDILKDWALLPGTKFTV}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      {	t RLKHLLLEIGFNLVYNCDETANLYHCLVDADIPVSYVTPADVRSFLMTFSSPDTNCHI}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GK ITDGDRLKRKQFHASV I DSVTKKRQLKD I PVQQ I TYTMDT EDSEGNLTTWL I CNRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RRLGLVPCGAVGVLLHETQEQKWTVKPHIGEVFCYLPLRIKTGLPIHINGCFAVTSNR
KEIWKTDTKGRWNTTFMRHVIVKAYLQALSVLRDLAIGGELTDYTYYAVWPDPDLVHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALNAPVLSVLKEAAKLMKTCSSSNKKLPTDVPKSSCILQITVEEFHHVFRRIADLQSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LDPNEMRTVKRVVSGLFKSLQNDSVKVRSDLENARDLALYLPSQDGKLVKSSILVFDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LESLLIIHDANNRLKQAKHFYDRTVRVFEVMLPEKLFIPKEFFKKLEQVIKPKNQAAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DFSVICKGFYEDIAHGKGKELTRVFSDGSMWVSMKNVRFLDDSILQRKDVGSAAFKIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           {	t LFRGPDDDPATLFEMAKSGQSKKPSDELPQKTVDCTTWLICTCMDTGEALKFSLNESG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NTADIYSLVDEFSLCGHRLIIFTQSVNSMYLKYLKIEETNPSLAQDTIIIKKKVCPSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QQKRLRKFPNQFKPFIDVFGCQLPLAVEAPYSYNGTLFRLSFRTQQEAKVSEVSSTCY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EVDKVGKFGLGFNSVYHITDIPIIMSREFMIMFDPNINHISKHIKDRSNPGIKINWSK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLKVPCLSTRLINPENMGFEQSGQREPLTVRIKNILEEYPSVSDIFKELLQNADDANA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFKACGSIEELTSDHISMVIQKVYLKSDQELSEEESKQNLHLMLNIMRWLYSNQIPAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     {	t TDTSEKEKRIIQELTIFKRINHSSDQGISSYTKLKGCKVLDHTAKLPTDLRLSVSVID}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLFDEMPLIPRTLLNEDQTCVELIRLRIPSVVILDDETEAQLPEFLADIVQKLGGIVL
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/translation="MNTFWPGRELVVQWYPFSEDKRHPSLSWLKMVWKNLYIHFSEDL
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RESULT 7
AC138718/c
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KEYWORDS
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TITLE
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                                                                                                                                                                                                                                                                                                                                             Chemistry: Dye-primer ET; 0% of reads Chemistry: Dye-terminator Big Dye; 100% of re Assembly program: Phrap; version 099319 Consensus quality: 282412 bases at least Q40 Consensus quality: 283029 bases at least Q30 Consensus quality: 283429 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Washington University Genome Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 283096)
McPherson, J.D. and Wat
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                                                                                                                                                                                                                                                                 Insert size: 218000; agarose-fp
Insert size: 286547; sum-of-contigs
Quality coverage: 18.55 in Q20 bases; agarose-fp
Quality coverage: 12.13 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center project name: M_BA0221F08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Web site:http://genome.wustl.edu/gsc/index.shtmlContact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-FEB-2003) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 1 to 283096)
McPherson, J.D. and Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus chromosome UNK clone RP23-221F8, WORKING DRAFT SEQUENCE, 4 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; 0% Sequencing vector: plasmid; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---- Genome Center ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkway, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (15-JAN-2003) Genome Sequencing Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence of Mus musculus clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC138718
AC138718.1 GI:27753855
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                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     musculus (house mouse)
     33705
33805
85934
86034
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     33804:
85933:
86033:
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contig of 33704 bp in 1 gap of unknown length contig of 52129 bp in 1 undnown length contig of 68220 bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 722)
Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Lander, E.S., Lindblad-Toh, K. and Daly, M.J.
The mosaic structure of variation in the laboratory m Nature 420 (6915), 574-578 (2002)
22354684
12466852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT
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                                       as STSs and 81,000~{\rm SNPs} were annotated with alleles from C57BL/6J and the strain from which the particular read came. The validation
                                                                                           WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 12951/SvImJ, C3H/HeJ, and BALB/cByJ. The WGS reads were placed uniquely on the MGSCV3 C57BL/6J assembly and SNI detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                       Tel:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus
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 rate for these SNPs was estimated at approximately 98%.
Location/Qualifiers
                                                                           annotated
                                                                                                                                                                                          STS size:
                                                                                                                                                                                                                                                                                                                                           Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BV018667.1
                                                                                                                                                                                                                Primer B:
                                                                                                                                                                                                                                                 Email: kersli@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                         320 Charles Street,
                                                                                                                                                                                                                                                                                                                           Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tagged site
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Similarity 73.9%;
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154354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="assembly_name:Contig52"
154354, .283096
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4 283096: contig of 128743 bp in
Location/Qualifiers
                                                                                                                                                                                            None
722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig53"
61811 c 61785 g 79513 t
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/chromosome="UNK"
/clone="RP23-221F8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Mus musculus"
/mol_type="genomic DNA"
                                                                                                                                                                                                                                None
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="assembly_name:Contig50"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GI:31102562
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Rodentia;
                                                                                                                                                                                                                                                                                                         Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 53.6; DB 2;
Pred. No. 4.7e-05;
0; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              722 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA
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STS 30-MAY-2003 sequence

Mullikin, J.C., Murinae; Mus 0;

Gaps

60

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STS
BASE COUNT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Benahmed,F., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A., Checko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregoorgis,B., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hines,S., Hladun,S., Haddeson,A., Hernandez,J., Hines,S., Hladun,S., Hodgson,A., Hernandez,J.,
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Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nayagan, M., Morris, S., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nankervis, C., Newton, G., Olarnpunsagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Puzzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R. Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Shenter, S., Scott, G., Shatsman, S., Shen, H., Shetty, T., Shenter, S., Scott, G., Shatsman, S., Shen, H.
                                                                                                                                                                                                                                                                                                                                                        Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuhewa, L., Loulseged, H., Lozado, R.J., Lu, X., Ma, J., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mawhiney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Norway rat)
Rattus norvegicus
Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus clone CH230-4E7, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus
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<1. .>7
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/map="+ 14 22-662 52304811-52305451"
/clone_lib="CZECHII/E1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="CZECHII/Ei"
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91.28;
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N PROGRESS ***,
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                                                                                                          Reigh, R.,
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TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steimle, M., Ströng, R., Suttön, A., Svatek, A., Tabor, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, Y., Yu, F., Zhaug, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Molecular and Human Genetics, Bay
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 240277)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   shotgun sequence only contigs will be indicated in the feature
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                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                 as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                 be preserved
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Consensus quality: 228324 bases at least Q40 consensus quality: 230109 bases at least Q30 Consensus quality: 230114 bases at least Q20 Estimated insert size: 240669; sum-of-contigs estimation Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                            239208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: hgsc-help@bcm.tmc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM
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/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                            ocation/Qualifiers
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misc_feature

complement(237792. .238683)

/clone="CH230-4E7"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J., Ferreira, P., FitzHugh, W., Forrest, C., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McDheeters, R., Meldrim, J., Meneus, L., Morrow, J., Naylor, J., McDheeters, R., Meldrim, J., Moneus, L., Morrow, J., Naylor, J., McDheeters, R., Meldrim, J., Maneus, L., Morrow, J., Naylor, J., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rothman, N., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Vassiliev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Janes, A., 2014, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Alle Anderson, S., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Boushaykiy, L., Boukhgalter, B., Brown, A., Burkett, G., Castle, Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65; Conserv
                                                                                                                                                                                                                                                                                                                                           Submitted (22-JAN-2000) Whitehead Institute/MIT Center for Research, 320 Charles Street, Cambridge, MA 02141, USA On Jul 13, 2000 this sequence version replaced gi:6730876. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zimmer, A. and Zody, M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren, B., Linton, L., Nusbaum, C. and Homo sapiens, clone RP11-21G21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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NOTE: This record contains 91 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAATCCAGTTAAAAAAACGGTATTTCCCTGGT 125254
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                                                                                                                         Center project name: L4008
Center clone name: 21_G_21
                                                                                                                                                                         Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                         Center code: WIBR Web site: http://w
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                                                                 Human protein tyrosine phosphatase;
Patent: WO 0160992-A 3 23-AUG-2001;
PE Corporation (NY) (US)
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AX350371
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Wei,M.-H., Ketchum,K.A., Di Francesco,V. and Beasley,E.M.

Isolated human phosphatase proteins, nucleic acid molecules

encoding human phosphatase proteins, and uses thereof

Patent: US 6479270-A 3 12-NOV-2002;
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AR253940
                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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/db_xref="taxon:9606"
14055 c 14307 g 2482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CNS01DXI 190648 bp DNA linear PRI 04-MAY-2001
Human chromosome 14 DNA sequence BAC R-589M4 of library RPCI-11
from chromosome 14 of Homo sapiens (Human), complete sequence.
                                                                                                                                                                                                                                                                                                                                            Assembly program: Phrap; version Quality coverage: 9.67x in Q20 ba
                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www.genoscope.cns.fr/
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center: Genoscope / Centre National de Center code: GS

    Web: www.genoscope.cns.fr)
    On May 8, 2001 this sequence version replaced gi:11611152.
    Genome Center

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (04-MAY-2001) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Heilig,R., Petit,J.L., Vico,V., Dasilva,C., Robert,C., Wi
Brottter,F., Cattolico,L., Barbe,V., Pelletier,E., Artigu
Levy,M., Eckenberg,R., Bruls,T., deBerardinis,V., Cruaud,
Gyapay,G., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                             Percentage
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                                                                                                                                                                                                                                                                                           Overall quality chart :
                                                                                                                                                                                                                                                                                                                                                                                           The following BAC sequence is oriented
                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: SeqRef@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
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/organism="Homo sapiens'
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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                                                            e of bases with a q
Location/Qualifiers
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Pred. No. 3.6;
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Cruaud,C.,
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Homo.
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         Muzny, D. Marie., Metzkér, M. Lee., Abramzon, S., Adams, C., All
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Angulano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benn
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,
                                                                                                                                                                                  Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                 ACO97744.9 GI:30521774
HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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                                                                                                                 Rattus.
1 (bases 1 to 291738)
                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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/note="matching
RHdb:RH44425
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Identified using the e-PCR software
37509 c 37884 g 57142 t
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RHdb:RH99190
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33101. .33202
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/note="matching EMBL:G30493
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Sciurognathi; Muridae;
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Harvey, Y., Haves, A., Henderson, N., Hernandez, M., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hegues, M., Hollins, B., Howells, S., Hulyk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Kovar, C., Kovar, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on May 10, 2003 this sequence version replaced g1:24818859.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                          contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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Direct Submission
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Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                       Center code: BCM
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REFERENCE AUTHORS

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JOURNAL

COMMENT

The sequence of Mus musculus clone

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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                               122903 GAAAAAGTTATTAACCTGGGTTTG 122926
                                                                                                                                                                                                                                                                                                                                                                                       72 AAAAACGGTATTTCCCTGGTTCTG
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                                                                                                                                                                                 156547 bp DNA linear
Mus musculus clone RP24-537M7, complete sequence.
AC117262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
53; Conserv
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 156547)
McPherson,J.D. and Waterston,R.H.
                                                                                             Mus musculus
                                                                                                                                           HTG
                                                                                                                                                              AC117262.2
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NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            as soon as it is available and the accession number will
                                                                                                                  musculus (house mouse)
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Center clone name: CH730-1114
Consensus quality: 220846 bases at least Q40
Consensus quality: 22734 bases at least Q30
Consensus quality: 224200 bases at least Q20
Estimated insert size: 230218; sum-of-contigs estimation
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251789. .252485
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/db_xref="taxon:10116"
/clone="CH230-11N4"
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clone_end:T7"
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                                                                     Direct Submission
Submitted (31-OCT-2002) Wellcome Trust Sanger Institute, Hinxton.
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Nov 1, 2002 this sequence version replaced g1:24414771.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59;
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
                                                               Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                       Bates, K.
                                                                                                                                                                                                                                                                                                                                                                                                      Mouse DNA sequence from clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT 60
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On May 16, 2002 this sequence version replaced gi:20069850.
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Submitted (21-MAY-2002) Genome Sequencing
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 156547)
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MCPherson,J.D. and Waterston,R.H.
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McPherson, J.D. and Waterston, R.H.
Direct Submission
Submitted (08-APR-2002) Genome Se
                                                 Center code: SC
                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                      sequence.
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2 (bases 1
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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Pred. No. 15;
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This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as Compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw:, SWISSPROT; TR:, TREMBL; WP:, WORMPEP; Information on the WORMPEP
                                                                        Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT
                      Center: Wellcome Trust Sanger Institute Center code: SC
                                                                                                                                                                                                  Submitted (07-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on May 10, 2003 this sequence version replaced gi:30550058.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus chromosome 2 PROGRESS ***, 3 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.
                                                                                                                                                                                                                                                                                                                       Direct Submission
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                                                                                                                                                                                                                                                                                                                                                Johnson,C
                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-446017 is
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                                                                                                                                                                                                                                                                                                                                                                   karyota; Metazoa; Chordata;
mmalia; Eutheria; Rodentia;
(bases 1 to 248044)
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/chromosome="2"
http://www.sanger.ac.uk
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36061 c 35495 g 53447
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33.8;
Pred. No. 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            248044 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone RP23-42M7,
                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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RESULT 18
AC134425/c
                                                                                                                                VERSION
KEYWORDS
                        REFERENCE
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ORIGIN
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  AUTHORS
                                                                                       ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                         61 AATACAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 172022)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT 60
                                                                                       Mus musculus
                                                                                                                           AC134425.3 GI:28927764
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chemistry: Dye-terminator; 100% of reads
Consensus quality: 247687 bases at least Q40
Consensus quality: 247768 bases at least Q30
Consensus quality: 247797 bases at least Q20
                                                                                                                                                                          AC134425
                                                                                                                                                                                              pieces
                                                                                                                                                                                                                Mus musculus clone RP24-266E5, WORKING DRAFT SEQUENCE, 5 unordered
                                                                                                                                                                                                                                           AC134425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     coverage: 11.39x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Insert size: 247844; sum-of-contigs
Insert size: 223039; 6.2% error; agarose-fp
Quality coverage: 10.25x in Q20 bases; sum-of-contigs Quality
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Assembly program: XGAP4; version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: humquery@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                 AGTATTTTCTATAAAATGGTATTTTAGAGGTTCTGAGTCAA 26708
                                                                                                                                                                                                                                                                                                                                                                                                                                 GTATTGCCTTTAGCAACATATTCATTTATTCATTGTTAACTATTGATCAAGTAATTTGGG 26749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           be preserved
                                                                                                     musculus (house mouse)
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168665
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/note-"assembly_fragment:03589"
4 48203 c 50482 g 76625 t
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fragment_chain:1"
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fragment_chain:1"
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/chromosome="2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clone_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               location/Qualifiers
Nusbaum, C. and Lander, E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 248044
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Pred. No. 15;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., MacLean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Mguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Tavers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA on Mar 12, 2003 this sequence version replaced gi:28275012. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren,B., Nusbaum,C., Lander,E., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavkly,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., FitzGerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Vell, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Topham, R., Wu, X., Wyman, D., Young, G., Zainoun, J., Well, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Topham, K., Travers, M., Vassiliev, H., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Topham, K., Travers, M., Vassiliev, H., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Topham, K., Travers, M., Vassiliev, H., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Young, G., Zainoun,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-SEP-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 172022)
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Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
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Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus, clone RP24-266E5
Unpublished
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                                                                                                                                                                                                                                      Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.960731
Consensus quality: 170825 bases at least Q40
Consensus quality: 171283 bases at least Q30
Consensus quality: 171504 bases at least Q20
Quality coverage: 9.2 in Q20 bases; agarose-fp Quality coverage: 9.4 in Q20 bases; sum-of-contigs
                                                                                                                      Insert size: 174000; agarose-fp
Insert size: 171622; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------ Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: 266_E_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center project name: L27143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT Center for Genome Research Center code: WIBR
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                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N
Direct Submission Submitted (15-NOV-2001) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                  HTG
                                                                                                                                                                                                                                                                               AC099520 180219 bp DNA Homo sapiens chromosome 5 clone RP11-6N13,
                                                      2 (bases 1 to 180219)
DOE Joint Genome Institute
                                                                                      Unpublished
                                                                                                          Direct Submission
                                                                                                                           DOE Joint Genome Institute and Stanford
                                                                                                                                         Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 180219)
                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                  AC099520.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                     ATACAGTTAAAAAACGGTATTTCCCTGGTTCTGATCCAACA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAGTCATTGAGAAAATAACTACCTGTCAGATTTTTTCAGCTACTGCTGATGGGAATTCTTA 72775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  consists of 5 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52893
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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20600. .35071
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172022: contig of 82342 bp
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gap of 100 bp
contig of 14472 bp in length
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contig of 54409 bp in length
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Pred. No. 22;
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                                                                                                                                                        Catarrhini; Hominidae; Homo.
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                                                                                                                                                                  Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Matthews, C., McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Nozbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P.,
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On Feb 26, 2002 this sequence version replaced gi:16930936.
Draft Sequence Produced by DOE Joint Genome Institute
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                                                                                               Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J. Tesfâye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                    Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastlen,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Camarata,J., Chang,J., Chazaro,B., Choppel,Y., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 202522)
Birren, B., Nusbaum, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus clone RP24-124H4,
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Location/Qualifiers
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                            Submitted
                                                Direct Submission
                                                                          Zembek,L.
                                                                                                                                                                                                                                                                                                                                                                                          Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus, clone RP24-124H4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC130698.3 GI:28913297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="5"
(13-AUG-2002) Whitehead Institute/MIT Center 320 Charles Street, Cambridge, MA 02141, USA
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30647 c 30821 g
                                                                        Zimmer, A. and Zody, M.
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57.8%;
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Pred. No. 22;
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24-124H4, WORKING DRAFT SEQUENCE,
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Sciurognathi; Muridae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (11-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 11, 2003 this sequence version replaced gi:28629909. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Boguslavkly,L., Boukhgalter,B., Camarata,J., Chang,J., Choepel,Y Collymore,A., Cook,A., Cooke,P., Corum,B., DeArellano,K., Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 (bases 1 to 202522
Birren, B., Nusbaum, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 198981 bases at least Q40

Consensus quality: 199528 bases at least Q30

Consensus quality: 199865 bases at least Q20

Insert size: 182000; agarose-fp

Insert size: 201522; sum-of-contigs

Quality coverage: 11.1 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
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Center clone name: 124_H_4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
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80212
80312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
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75160:
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74354: gap of 100 bp
                                                                                                                                                                                                                                                                                                            contig of 706 bp in length gap of 100 bp contig of 662 bp in length gap of 100 bp
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contig of 2601 bp in
                                                                                                                                                                                                                                                                                       contig of 1588 bp in length
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of 100 bp
in of 3752 bp in length
of 100 bp
ig of 8280 bp in length
of 100 bp
ig of 22040 bp in length
of 100 bp
ig of 15788 bp in length
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AUTHORS
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                                                     Contact: Kerstin Lindblad-Toh
                                                                                                             Unpublished (2002)
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                       Whitehead Institute for Biomedical Research, Center
                                                                                                                                       Polymorphism Structure
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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130572. .200457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:10090"
/clone="RP24-124H4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                       GI:22754019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . 20252
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200457: contig of 69886 bp in length
200557: gap of 100 bp
200552: contig of 1965 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32.2%;
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Pred. No. 2
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HS1110P6/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
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AL Submitted (21-MAY-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: Clonerequest@sanger.ac.uk
On May 25, 2002 this sequence version replaced gi:5101738.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 ATACAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Primer A: None
Primer B: None
STS size: 554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HS1110P6 40033 bp DNA 1110P6 on Clone RP5-1110P6 on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and the strain from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 as STSs and 81,000 SNPs were annotated with alleles from C57BL/6J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WGS-discovery: Paired-end low-coverage whole genome shotgun reads were generated from 129S1/SVImJ, C3H/HeJ, and BALB/CByJ. The WGS reads were placed uniquely on the MGSCV3 C57BL/GJ assembly and SNP detection was carried out by SSAHA-SNP. 225,000 reads were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AL049175.12 GI:21212890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAAAAGTTAAAAGAACTTTAACTCCATTATTGTAACTCCA 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAAAAATTAAAATATTTTAAAAAAGCAGCTATCATAGGTCATGCCTTAGGTAATTTAAA 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 40033)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Charles Street, Cambridge, MA 02141, USA
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/map="- 19 22-495 22440264-22440739"
/clone_ib="C3H/HeJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="C3H/HeJ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
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78 c
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              42;
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n chromosome
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SOURCE
ORGANISM
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AC141553
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Best Local
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Allen,C., Allen,H., Alsbrooks,S., Amin,A. Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceassar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Cree,A., D'Souza,L.,
Chacko,J., Chavez,D., Chen,G., Coyle,M., Cree,A., D'Souza,L.,
Chacko,J., Chavez,D., Chen,G., Coyle,M., Cree,A., D'Souza,L.,
Claveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Elugene,C., Evans,C.A., Falls,T., Fan,G.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,B., Geer,K., Gill,R., Gracia,A., Garner,T., Garza,M.,
Gebregeorgis,B., Geer,K., Gill,R., Gracia,A., Garner,T., Garza,M.,
Gebregeorgis,B., Geer,K., Gill,R., Gracia,A., Garner,T., Garza,M.,
Gebregeorgis,B., Geer,K., Hamail,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hollins,B., Howells,S., Hulwk,S., L., Hodgson,A., Hogbes,M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39156 CAACTGGCATTTTCCAGATTCTAA 39133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39216 ATTCCAAGTTAAATACAGCATGTTTCCCACTTTCTTTTGGGACATGATAGTACTGTTAGG 39157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    73 AAAACGGTATTTCCCTGGTTCTGA 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156493 bp DNA linear HTG 17-MAR-2003 Rattus norvegicus clone CH230-123N13, *** SEQUENCING IN PROGRESS ***, 71 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://www.sanger.ac.uk/HGP/ChrX
RP5-1110P6 is from the library RPCI-5 constructed by the group of
Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny,D.Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC141553.1 GI:28975844
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Submitted (17-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                          arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                         (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 71 contigs. The true order of the pieces is not known and their order in this sequence record is
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be preserved.
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Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Steinle, M., Strong, R., Sutton, A., Svatek, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walter, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczyk, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhoo, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
                                AL Submitted (20 Nov-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced g1:23266189.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature
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JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAL

Center project name: GOYF
Center clone name: CH230-18504
Center clone name: CH230-18504
Center clone name: CH230-18504
Center Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 186401 bases at least Q30
Consensus quality: 189924 bases at least Q30
Consensus quality: 192483 bases at least Q30
Consensus quality: 192483 bases at least Q30
Estimated insert size: 189616; sum-of-contigs estimation Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM Quality coverage: 6x in Web site: http://www.hgsc.bcm.tmc.edu/ -- Genome Center Q20 bases; sum-of-contigs

NOTE: Estimated insert size may differ from sequence length (see http://www.bgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs

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REFERENCE
AUTHORS
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Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Center,A.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Chaveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
                                                                                                                                                 1 (bases 1 to 252839)
Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Al.
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Ben
Biswalo, D., Bart T., Barnstead, M., Ben
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC095096 252839 bp
Rattus norvegicus clone CH230-7G9,
                                                                                                                                                                                                                                                                               Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                               Rattus.
                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
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1 209701: contig of 209701 bp in length.
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a 42541 c 42380 g 52735 t 15590 others
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clone_end:T7
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complement(208485.
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101254. .102704
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102916. .103994
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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Pred. No. 32;
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Murinae;
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В

REFERENCE AUTHORS

JOURNAL TITLE

COMMENT

Center project Information Center clone name: CH230-7G9

Web site: http://www.hgsc.bcm.tmc.edu/Contact: hgsc-help@bcm.tmc.edu Center: Baylor College of Medicine Center code: BCM JOURNAL REFERENCE

TITLE

AUTHORS TITLE

JOURNAI

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Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Ngupen, N., Norris, S.,
Nwaokelemeh, O., Okwuonu, G., Olarnpunsagoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Poloper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Plopper, F., Polindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
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Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
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Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
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Shetty, J., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shen, H., Sosa, J.,
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Shetty, J., Shen, H., Sosa, J., Wang, J.,
Wang, G., Walton, A., Svatek, A., Tabor, P., Taylor, C.,
Wallams, G., Willson, R., Walter, R., Walter, B., Wang, J.,
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Walter, B., Walter, R., Walter, B., Wang, J.,
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Walter, B., Walter, B., Shetty, B., Wooden, H., Worley, K.,
Walter, B., Walter, B., Shetty, B., Walter, B., Walter, B.,
Walter, B., Walter, B., Walter, B., Walter, B.,
Walter, B., Walter, M., Shetty, B., Walter, B.,
Walter, B., Walter, B., Walter, B.
                                                                                                                                                                                                     Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 9, 2003 this sequence version replaced g1:24818178.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 252839)
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Direct Submission
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Hernandez,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T.,
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RESULT 26
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blawalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Cocyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Dedgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Decaro, C., Ding, Y., Dinh, H., Divya, K., Decaro, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Decaro, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Decaro, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Davis, C., Decaro, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Davis, C., Decaro, C., Ding, Y., Dinh, H., Divya, K., Davis, C., Dav
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC118378
AC118378.4 GI:23618102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus clone CH230-35816, *** SEQUENCING ***, 2 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC118378
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(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently
consists of 3 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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250042
251415
251515
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Assembly program: Atlas;
Consensus quality: 248637 bases at least Q40
Consensus quality: 249895 bases at least Q30
Consensus quality: 250757 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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54152 c 55812 g 69248 t
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/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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REFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Web site: http://www.hgsc.bcm.tmc.edu/ Center: Baylor College of Medicine JOURNAL REFERENCE

TITLE

AUTHORS TITLE JOURNAL

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Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garca, M., Gabrer, T., Garza, M., Gebregoorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gubrerorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, M., Hollins, B., Howells, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hallyk, S., Khan, Z., King, L., Kovar, C., Vargathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensuheva, L., Louiseged, H., Lozado, R.J., Lu, X., Ma, J., Waheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mahmoud, M., Malloy, K., Mangum, A., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Milosavijevic, A., Miner, G., Mindas, M., Murphy, M., Nair, L., Moore, S., Mundesta, M., Murphy, M., Nair, L., Mangum, A., Wangervis, C., Nodev, T., Noverin, N., Nguyen, N., Norris, S., Nankevis, C., Paul, H., Perez, A., Perez, L., Prannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L., Plage, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Sinter, C., Shatsman, S., Shen, H., Shet, J., Shen, J., Sutton, A., Svatek, A., Tabor, P., Taylor, C., Taylor, C., Wang, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Warren, J., Wooden, H., Worley, K., Waillag, R., Smith, D., R., H
                                    and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (11-OCT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Oct 9, 2002 this sequence version replaced gi:21746207. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (17-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
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shotgun sequence only contigs will be indicated
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KEYWORDS
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                                                                                                                                RESULT 27
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                                                                                                                                                                                                                                                                                                                                    53,
                  AC121737
AC121737.4 GI:25138094
                                                                       Rattus norvegicus clone
                                                                                                                                                                                                                                                                                                                                                     Similarity
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                    unordered pieces.
                                                                                                                                                                                                                     AACGGTATTTCCCTGGTTCTGATCCAA 101
                                                                                                                                                                                                                                                                                         AACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAAAA 74
                                                                                                                                                                                   ATCTGTATTTCCCATGTCCTATTCCTA 225107
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   HTGS_PHASE1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="wgs_con__
                                                                                                                                                                                                                                                                                                                                                                                                                         end_sequence:RXATN51TVB"

4 43661 c 43433 g 54154 t
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complement(252911.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-35816"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="clone_boundary
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clone_end:T7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="clone_boundary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence: RXATN51TJB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255030: contig of 255030 bp in length 255130: gap of unknown length 256498: contig of 1368 bp in length.
                                                                                                                                                                                                                                                                                                                                                  31.7%;
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HTGS_DRAFT; HTGS_ENRICHED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       _contig"
                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                Score 32.6;
Pred. No. 31;
                                                                       263259 bp
ne CH230-74A9,
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                                                              DNA linear
, *** SEQUENCING
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                                                       Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Nov 20, 2002 this sequence version replaced gi:22856055. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-MAY-2002) Human Genome of Molecular and Human Genetics, Bayl Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 263259)
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Mankervis,C., Neal,D., Newton,N., Nuyven,N., Norris,S.,
Nwaokelemeh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Rejfer,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,R., Ruiz,S.J.,
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorella,R., Sosa,J.,
Steimie M., Strong, R., Sutton, A., Systek, A., Tahor, D.,
Steimie M., Strong, R., Sutton, A., Systek, A., Tahor, D.,
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Strong, R., Sutton, A., Systek, A.,
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Ben,
Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
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Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baylor College of Medicine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Benahmed, F.,
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RESULT 28
AP004386/c
LOCUS
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ORIGIN
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      AP004386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces
                                                                                                                                                AACGGTATTTCCCTGGTTCTGATCCAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                        ATCTGTATTTCCCATGTCCTATTCCTA 105026
                                                                                                                                                                                                                              AACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAAAA 74
                                                                                                                                                                                                                                                                                                                                                                                   69680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as soon as it is available and the accession number will be preserved.
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257814
258997
258997
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Consensus quality: 233743 bases at least Q40
Consensus quality: 237630 bases at least Q30
Consensus quality: 239718 bases at least Q20
Estimated insert size: 239635; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             261188
261288
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Center code: BCM
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54257 c 54754 g
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
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261287: gap of unknown
263259: contig of 1972
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Pred. No. 3:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (30-NOV-2001) Nobuyoshi Shimizu, Keio University, So of Medicine, Molecular Biology; 35 Shinanomachi, Shinjuku-ku, 160-8582, Japan (E-mail:nshimizuedmb med.keio.ac.jp, Tel:81-3-3351-2370, Fax:81-3-3351-2370) On Feb 2, 2002 this sequence version replaced gi:17298203.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens genomic DNA, AP004386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shimizu, N. and Asakawa, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimizu, N. and Asakawa, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AP004386.2 GI:18479066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Published Only in Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens DNA chromosome
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complement(2231. .3770)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1984. .2203)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(5. .1942)
                                                                                                                                                                                                                                                                                                complement(9511. .9633)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(5011. .5364)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpt_family="(TG)n"
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                                                                                                                                                                   .10625
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19944. .1998!
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complement(28605..28709)
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complement(26527. .26641)
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/rpt_family="MIR"
30453. .30714
                                                                                                    27141. .27268
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/rpt_family-"L1P1"
complement(26421...26492)
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complement(17787. 17901)
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30873. .30893
                                                                                                                                                                                                                complement(28842. .28967)
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/rpt_family="MIR"
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| RESULT 29 AL954648/C AL954648 LOCUS DEFINITION Danio rerio unordered p ACCESSION AL954648 | Qy 65 CAGTTA Db 138173 CACTTT | . Qy 5 TGACTG Db 138233 TCACTA | Query Match Best Local Similarity Matches 51; Conser | repeat_region | repeat_region | repeat_region | repeat_region | repeat_region | rebear_redion | | repeat_region | repeat_region | | repeat region | repeat_region | | | repeat_region | repeat_region | repeat_region | | repeat_region | repeat_region | repeat_region | |
|---|---|--|---|--|--|---|---|--|---|--|--|--|---|---|--------------------------------|---|---|--|-------------------------------|--|---|----------------------------------|--|--|--|
| 167153 bp DNA linear o clone CH211-245P24, *** SEQUENCING IN pieces. | CAGTTAAAAAAACGGTATTTCC 86 | TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA | 31.5%; Score 32.4; DB 9; Length 159598; ilarity 62.2%; Pred. No. 38; Conservative 0; Mismatches 31; Indels 0; | /rpt_ranlly="Mik" 45494. 45527 /evidence=not_experimental /rpt_family="(T)n" | <pre>/rpt_family="AT_rich" complement(4320743335) /evidence=not_experimental</pre> | /rpt_family="(TG)n" 4260042621 /evidence=not_experimental | /rpt_ramlry="Mik" 42309. 42364 /evidence=not_experimental | 4208142308 /evidence-not_experimental | <pre>comprement(41043. 41/39) /evidence=not_experimental /rot_family="L2"</pre> | /evidence=not_experimental /rpt_family="L2" | <pre>/rpt_family="L2" complement(4102041115)</pre> | <pre>complement(4078940984) /evidence=not_experimental</pre> | <pre>/evidence=not_experimental /rpt_family="(CA)n"</pre> | /evruence-not_experimental /rpt_family="CT-rich" 3815738188 | /+pc_ramity="12" 3695537043 | complement(3658536717) /evidence=not_experimental | /evidence=not_experimental /rpt_family="(CAAA)n" | /rpt_family="AluYb8" /rpt_family="AluYb8" 35940, 35964 | /rpc_remity="HALL" 3567235935 | 3191232467 /evidence=not_experimental | <pre>/evidence=not_experimental /rpt_family="AluSx"</pre> | /rpt_family="HAL1" 3161231911 | 31330. 31611 // Sevidence=not_experimental | 3108631241 /evidence-not_experimental /rot_family="HAL1" | <pre>/evidence=not_experimental /rpt_family="(A)n"</pre> |
| HTG 12-MAR-2003 PROGRESS ***, 2 | | CTAATA 64 CTTCTG 138174 | Gaps 0; | | | | | | | | | | - | | | | | | | | | | | | |

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AUTHORS
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                                                                                                                                                                                                                                                                                                   BASE COUNT
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                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
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                                                                                                                                                                                                        Local Similarity
20384 GTTCTGTGGGTCTCATCTAGCA 20363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (08-MAR-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Mar 13, 2003 this sequence version replaced gi:27652871.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
----- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cyprinidormes; Cyprinidae; Danio.

1 (bases 1 to 167153)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Insert size: 167053; sum-of-contigs
Insert size: 168747; 7.2% error; agarose-fp
Quality coverage: 8.21x in Q20 bases; sum-of-contigs Quality
coverage: 8.13x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Consensus quality: 166934 bases at least Q40 Consensus quality: 166970 bases at least Q30 Consensus quality: 166989 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Assembly program: XGAP4; version 4.5 Chemistry: Dye-terminator; 100% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center project name: zC245P24
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HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP
                                           TTTCCCTGGTTCTGATCCAACA 103
                                                                                                                                 TGATGGCAGCTTAAAGACATCTCTCATATATGACTTCAACAGAGAGTAAAAATCTTGATA 20385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130191
                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                         vector_side:left"
130291. .167153
                                                                                                                                                                                                                                                                                                                                          clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                       clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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/clone="CH211-245P24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1. .167153
                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment:00984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Danio rerio
                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="assembly_fragment:01240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ocation/Qualifiers
                                                                                                                                                                                                                                                                                            ector_side:right"
29865 c 29691 g
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130290: gap of 100 bp
167153: contig of 36863 bp in length.
                                                                                                                                                                                                      31.5%;
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                                                                                                                                                                                 0;
                                                                                                                                                                                                      Score 32.4;
Pred. No. 3
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REFERENCE
AUTHORS
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                                                                                                                         REFERENCE
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                                                                  AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                        Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lanazares, R., Landers, T., Lehoczky, J., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Milenga, V., Murphy, T., Naylor, J., Muyen, C., Nicol, R., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Well, D., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Well, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, M., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Vashou, T., Firmer, A. and Tody, M.
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O'Connor.T., O'Donnell.P., O'Neil.D., Oliver.J., Peterson.K.,
Phunkhang.P., Pierre,N., Pollara,V., Raymond,C., Retta.R.,
Phunkhang.P., Rise,C., Rogov.P., Roman.J., Rosetti,M.,
Rieback.M., Riley.R., Rise,C., Rogov.P., Roman.J., Rosetti,M.,
Roy,A., Santos,R., Schauer,S., Schupback.R., Seaman,S., Severy.P.,
Roy,A., Santos,R., Schauer,S., Schupback.R., Stojanovic,N.,
Stogunez,C., Spencer,B., Stange-Thomann,N., Stojanovic,N.,
Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J.,
Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A.,
Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J.,
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Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 197877)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Anderson,S., Barna,N., Bastien,V., Bloom,T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkly,L.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S Barna,N., Bastien,V., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Choepel,Y., Collangelo,M., Collins,S., Collymore,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Collymore,A., Cooke,P., Dearellano,K., Dewar,K., Dearellano,K., Dewar,K., Dearellano,K., Dearellano,K., Dearellano,K., Dewar,K., Dearellano,K., 
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Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                      Research,
                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                               Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
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Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K.,
McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
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                                                                                                                                                                         320 Charles Street, Cambridge,
                                                                                                                                                                                                                                            (22-MAR-2002) Whitehead Institute/MIT Center for Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nusbaum, C., Lander, E., Allen, N., Anderson, S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197877 bp
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                                                      Ali, A., Allen, N.,
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Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A

Campopiano, A., Chang, J.,

Boguslavkiy, L.,

Ferreira, P., FitzHugh, W.,

COMMENT TITLE JOURNAL

Center code: WIBR

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McCarthy, M., McEwan, P., McKernan, K., Meldrim, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., VO, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 22, 2002 this sequence version replaced gi:14150949. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Web site: http://www-seq.wi.mit.edu
                                                                                                 complement(9221. .9531)
/rpt_family="AluJb"
                                                                                                                                                                                                                                         /rpt_family="AT_rich" complement(7673. .797)
                                                                                                                                                                                                                                                                                                                       /rpt_family="AluSp"
complement(4471...4
                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="L2"
complement(4068. .4116)
/rpt_family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="8"
                                             complement(9818.
                                                         complement(9749. .9800)
/rpt_family="MLT2C2"
                                                                                                                                                              complement(9110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="RPCI-11 Human Male BAC"
1237. .1283
                                                                                                                                                                                                                          rpt_family="Alusx"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rpt_family="(CA)n"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="RP11-200A13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family="(A)n"
                                                                                                                 _family="(TA)n"
                      family-"MLT2B3"
                                                                                                                                                                                 family="L1MB8"
                                                                                                                                                                                                                                                                                  ly="MLTlJ"
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                                           10124)
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RESULT 31
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                                                                                                                                                                                       5 TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA 64
                                                                                                                                                      TCACTAGAATGTCAGTTCCATGACAGCAAGATTTTGTCTTGTTCATCTTTTTAGCTTCTG 42296
                                                                          CACTTTAAACTACATTTTTTCC 42318
                                                                                                                                                                                                                                       Conservative
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complement(21255. .
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/note="< 30 qual SNGL region"
20363. 20535
                                                                                                                                                                                                                                                                                                               /rpt_family="AT_rich"
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complement(18029. .18044)</pre>
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complement(14392. ...
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complement(11539.
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complement(10209..10
/rpt_family="MLT2B3"
10726..10833
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complement(16653. .16659)</pre>
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/note="<30 qual SNGL region"
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15935. .15961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="<30 qual SNGL region"
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|6098. .16146
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                                                                                                                                                                                                                                                       31.5%; 62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _family="MER5B"
                                                                                                                                                                                                                                                                                                                                                      _family="MLT2B1"
                                                                                                                                                                                                                                                                                                                                                                                             _family="(TG)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       _family="MLT2B1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _family="(CATATA)n"
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                                                                                                                                                                                                                                                       Score 32.4;
Pred. No. 37;
                                                                                                                                                                                                                                     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 190387 bases at least 040
Consensus quality: 193248 bases at least 030
Consensus quality: 194812 bases at least 020
Insert size: 188000; agarose-fp
Insert size: 196776; sum-of-contigs
Quality coverage: 4.45 in Q20 bases; agarose-fp
Quality coverage: 4.27 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (18-MAY-2000) Genome Sequencing Center, Washing University School of Medicine, 4444 Forest Park Parkway, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 198176)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC069127

198176 bp DNA 1:
Homo sapiens chromosome 8 clone RP11-200A13,
SEQUENCE, 15 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing vector: M13; 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: H_NH0200A13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston, R.H.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC069127.1 GI:7923969
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                                                                                                                                                                                                                                                                             runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 15 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 198176)
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85018
85118
                                                             27448
33890
33990
50272
50372
66237
                                                                                                                                                                                        16049
16149
21739
                                                                                                                                                                                                                                     10685
                                                                                                                                                                         21839
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                                                                                                                                                                                                                                                      1078
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                                                                                                                                                                                                                                                                                                               contig of 1104 bp in length
gap of unknown length
contig of 1527 bp in length
gap of unknown length
                gap of
contig
gap of
contig
                                                                                                         gap of
                                                                                                                                          gap of
contig
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                                                                                                                                                                                                      gap of contig
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g of 15865 bp in
f unknown length
g of 18681 bp in
f unknown length
g of 17995 bp in
f unknown length
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of 6442
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of 5509
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of 5590
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of 5264
                                                                                                         unknown length of 16282 bp in
                                                                                                                                                                                                                                                                                   unknown
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arkway, St. Louis,
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                                                                                                                                                                                                      27945
                                                                                                                                                                                                                                    65
                                                                               205394 bp
Danio rerio clone CH211-223J10,
unordered pieces.
AL954337
                                                                                                                                                                                                                                                                                                                               51;
                                          AL954337.7 GI:29786487
HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT;
              Danio rerio (zebrafish)
Danio rerio
                                                                            AL954337
                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                     CACTTTAAACTACATTTTTTCC 27966
                                                                                                                                                                                                                                  CAGTTAAAAAAACGGTATTTCC 86
                                                                                                                                                                                                                                                                                                TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA 64
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162024. 198176
/note="assembly_name:Contig30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig27"
103213. .132684
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16149 .21738
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clone_end:T7
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/db_xref="taxon:9606"
/chromosome="8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_name:Contig28"
132785. .161923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27448.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_name:Contig21"
21839. .27347
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="assembly_name:Contig23"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="assembly_name:Contig22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=_"assembly_name:Contig19"
10785. .16048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_name:Contig26"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="assembly_name:Contig24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_name:Contig18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="RP11-200A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lone_end:SP6
Metazoa; Chordata; Craniata;
                                                                                                                                                                                                                                                                                                                                                                                                            36068 c
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                                                                                                                                                                                                                                                                                                                                                                                                          embly_name:Contig30"
35579 g 63011 t
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Pred. No. 37;
0; Mismatches
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 Vertebrata; Euteleostomi;
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PROGRESS ***, 2
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TITLE
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Best Local
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                                                                                                        194930
                                                                                                                                                                                        194990
                                                                                                                                              82
                                                                                                                                                                                                                      22 TAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAAAAAACGGTA 81
    AC021546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 205294; sum-of-contigs
Insert size: 207449; 7.7% error; agarose-fp
Quality coverage: 10.18x in Q20 bases; sum-of-contigs Quality
coverage: 10.49x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chemistry: Dye-terminator; 99% of reads Chemistry: Dye-primer Big Dye; 0% of reads Consensus quality: 205262 bases at least Q40 Consensus quality: 205273 bases at least Q30 Consensus quality: 205273 bases at least Q20 Consensus quality: 205282 bases at least Q20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  zfish-help@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Apr 10, 2003 this sequence version replaced gi:29561800.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center project name: zC223J10
----- Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 205394)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cambridgeshire, CB10 1SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (02-MAY-2003) Wellcome Trust Sanger Institute, Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Assembly program: XGAP4; version 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                   GTTCTGTGGGTCTCATCTAGCA 194909
                                                                                                                                          TTTCCCTGGTTCTGATCCAACA 103
                                                                                                                                                                                  TGATGGCAGCTTAAAGACATCTCTCATATATGACTTCAACAGAGAGTAAAAATCTTGATA 194931
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be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown This record will be updated with the finished sequence
                                                                                                                                                                                                                                                                                                                                                                           64629 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4047
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                                                                                                                                                                                                                                                                                                                                                                /note="assembly_fragment:01167
fragment_chain:1"
37468 c 37450 g 65746 t
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/db_xref="taxon:7955"
/clone="CH211-223J10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="assembly_fragment:02034"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="CHORI-211"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Danio rerio"
                                                                                                                                                                                                                                                                                      31.5%;
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4146: gap of 100 bp
205394: contig of 201248 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                    205394
                                                                                                                                                                                                                                                                                      Score 32.4;
Pred. No. 37;
207756 bp
                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                         DB 2;
  DNA
                                                                                                                                                                                                                                                                 31;
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linear
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PRI 29-JUN-2001
                                                                                                                                                                                                                                                                 Gaps
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AUTHORS
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SOURCE
FEATURES
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ACCESSION
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                                                     Center project Information
                                    Center clone name: 574_0_7
                                                                                             Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                    Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sapiens
                                                                                                                http://www-seq.wi.mit.edu
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Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McPhaeters, R., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Neyen, C., Norbu, C., Norman, C. H., O'Connell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Severy, P., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zannoun, J., Zembek, L., Zimmer, A. and Zody, M.
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                                                                                                                                                                                                      Submitted (29-JUN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 17, 2001 this sequence version replaced gi:13518209. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
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Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A.,
                                                                    http://ftp.genome.washington.edu/RM/RepeatMasker.html
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 ACO21546
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Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Center: Whitehead Institute/ MIT Center for Genome Research
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10040. 10111
/rpt_family="LIMB4"
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complement(22974. .24
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complement(15747. .16082)
/rpt_family="AluSx"
16212. .16597
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/rpt_family="MER5A"
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/rpt_family="Alusp"
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complement(20683..210
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complement(4030. .4)
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complement(31797. .32731)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (26-JUN-2002) Whitehead Institute/MIT Center Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               McCarthy, M., Meldrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Smith, G., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
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Direct Submission
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Direct Submission
Submitted (21-FEB-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Feb 3, 2002 this sequence version replaced gi:18308880.
On Feb 3, 2007 This sequence resion replaced gi:18308880.
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Sulston,J.E. and Waterston,R.
Toward a complete human genome sequence Genome Res. B (11), 1097-1108 (1998)
99063792
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Submitted (03-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St.
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Submitted (18-DEC-2001) Genome
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                                        Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Center project name: H_NH0383P06
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest. This sequence was finished as follows unless otherwise noted:

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. MO. For additional information about the map position of this sequence, see http://genome.wustl.edu/gsc Louis

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and Coworkers at http://www.chori.org VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-653B19; the clone sequenced to the right is RP11-332H14. Actual start of this clone is at base position RP11-383P6

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                                                                                 note="match to EST AA569191
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
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'note="similar_to
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AC026733.5 GI:15187255
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(NID:g14885424)"
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/note="similar to Homo
/no1:98483061)"
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12533. .12572
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                                                2 (bases 1 to 157331)
Baltren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, M., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Colangelo, M., Collins, S., Collymore, A., Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Contino, M., Donelan, L., Doyle, M., Collymore, A., Collymore, Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Collymore, Cocke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Collymore, Cocke, P., Deare, C., Cocke, P., Cocke, P., Deare, C., Cocke, P., Deare, C
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Submitted (25-JAN-2001) DOE Joint (
Drive, Walnut Creek, CA 94598, USA
4 (bases 1 to 132120)
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On Aug 15, 2001 this sequence version replaced gi:12484318.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens, clone RP11-2G21
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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56; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Finishing Completed at Stanford Human Genome Center www-shgc.stanford.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC015774.4
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HTGS_PHASE1; HTGS_DRAFT
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/mol_type="genomic DNA"
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/chromosome="5"
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, FitzHugh,W., Forres Gardyna,S., Grant,G
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                                  Funke, R., Gage, D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Tirrell, A., Vassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Manney, R., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Wassillev, H., Wassillev, H., Wassillev, H., Vo, A., Wheeler, J., Wu, X., Wassillev, H., Wassillev, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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Insert size: 156031; sum-of-contigs
Quality coverage: 4.7 in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Assembly program: Phrap; version 0.960731
Consensus quality: 150588 bases at least Q40
Consensus quality: 153615 bases at least Q30
Consensus quality: 154711 bases at least Q20
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Sequencing vector: Plasmid; n/a; %-0.f%% of reads
3.10880829015544Chemistry: Dye-terminator Big Dye;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center project name: L1523
Center clone name: 2_G_21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality cove.
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of 4556 bp in
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AC103561
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Waterston, R.H.

Direct Submission
Submitted (28-NOV-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 172387)
Waterston, R. H.
                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                        HTG;
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Homo sapiens chromosome UNK clone RP11-381012,
PROCRESS ***, 29 unordered pieces.
                                                                                     Unpublished
                                                                                                   The sequence of Homo sapiens clone
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AC103561.1 GI:17136164
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120263. .157331
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75359. .92799
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11495. .14270
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/mol_type="genomic DNA"
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sequencing vector: M13; 0%
sequencing vector: plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of re
Assembly program: Phrap; version 0.990319
Consensus quality: 159141 bases at least 040
Consensus quality: 162137 bases at least 030
Consensus quality: 164330 bases at least 020
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26778: contig
26878: gap of 1
29564: contig
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34209: gap of 3
34309: gap of 3
36982: contig
37082: gap of 3
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="UNK"
                                                                                                                                         note≃"assembly_name:Contig34'
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contig of 19801 bp in length
gap of unknown length
contig of 27936 bp in length
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 CGGTATTTCCCTGGTTCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Howland, J.C., Illey, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheeters, R., Meldrim, J., Meneus, L., Mihova, T., Miranda, C., Mienga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Olivar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pisani, C., Pisani, C., Pisani, C., Pisani, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pisani, C., Pisani, C., Pisani, C., Pisani, C., Riley, R., Rogov, P., Rothman, D., Pisani, C., Pisani,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Birren,B., Linton,L., Nusbaum,C. and Lander,E. Homo sapiens chromosome 2, clone RP11-61701
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC062005 191682 bp
Homo sapiens chromosome 2 clone
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                                                                                                                                                                                                                                                                               All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                       On Oct 20, 2001 this sequence version replaced gi:10835354
                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Grand-Pierre, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Campopiano, A., Castle, A., Cnoepeu, I., Carryero, I., Cooke, P., DeArellano, K., Deary K., Diaz, J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Boguslavkiy,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC062005.3 GI:16303514
                                                                                                                                                                                                                                                 http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                     Research,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            roung, G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3alagan,J., Gardyna,S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 191682)
                                                                                                        Contact: sequence_submissions@genome.wi.mit.edu
                       Center clone
                                               Center project name: L9933
                                                                                                                                         Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                Center code: WIBR
                                                                                                                                                                                                 Center: Whitehead
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Santos, R., Schauer, S., Severy, P., Spencer, B.,
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171025. .172387
/note="assembly_name:Contig7"
a 37184 c 36658 g 48375 t
                                                                                                                                                                                                                                                                                                                                                                  320 Charles Street, Cambridge, MA 02141,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domino, M., Doyle, M., Ferreira, P., FitzHugh, W., Gage, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zainoun, J., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                (21-APR-2000) Whitehead Institute/MIT Center for Genome
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                                                                                                                                                                                                                            -- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unordered pieces
                                                                                Project Information
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                                                                                                                                                                                                 Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RP11-61701 map
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map 2,
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Graham, L.,

Ye, W.J.,

WORKING DRAFT HTG

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Gaps

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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality coverage: 5.9 in Q20 bases; agarose-fp Quality coverage: 5.6 in Q20 ba.

NOTE: This is a 'working draft' sequence. It currently consists of 14 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Consensus quality: 186043 bases at least Q40 Consensus quality: 188508 bases at least Q30 Consensus quality: 189610 bases at least Q20
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85732
85832
103758
103858
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125811
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173986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequencing vector: M13; M778
Sequencing vector: Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Insert size: 190382; sum-of-contigs
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51537
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17389
18866
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   /note="assembly_fragment"
43366. .51536
                                      /note="assembly_fragment"
34696. .43265
                                                                                                                                                  20368
                                                                                                                                                                                   /note="assembly_fragment"
18966. .20267
                                                                                                                                                                                                                                      vector_side:left"
                                                                                                                                                                                                                                                             clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
                                                                          25514
                                                                                                                         /note="assembly_fragment"
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                                                                                                                                                                                                                           17389
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                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11 Human Male BAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85731: contig of 34095 bp in length
85831: gap of 100 bp
103757: contig of 17926 bp in length
103857: gap of 100 bp
125710: contig of 21853 bp in length
125810: gap of 100 bp
147528: contig of 21718 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                .191682
                                                                                                                                                                                                                                                                                                 .17288
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17388: gap of 100 bp
18865: contig of 1477 bp in length
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contig of 17597
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contig of 2764 bp in
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of 26357 bp
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of 8171 bp in length
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of 9082 bp in
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                                                                                       Chemistry: Dye-terminator; 100% of reads consensus quality: 204770 bases at least Q40 consensus quality: 206949 bases at least Q30 consensus quality: 208949 bases at least Q20 Insert size: 212065; sum-of-contigs Insert size: 210479; 9.8% error; agarose-fp Quality coverage: 4.59x in Q20 bases; sum-of-contigs Quality coverage: 4.81x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     214165 bp
Danio rerio clone DKEY-32I12, ***
unordered pieces.
BX469976
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                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (01-MAY-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 15A, UK. E-mail enquiries: zfish-help8sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On May 2, 2003 this sequence version replaced gi:30142560.
             * NOTE: This is a 'working draft' sequence. It currently * consists of 22 contigs. The true order of the pieces * is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                           Web site: http://www.sanger.ac.uk
Contact: zfish-help@sanger.ac.uk
-----Project Information
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                                                                                                                                                                                                                                                   Assembly program: XGAP4; version 4.5
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1. (bases 1 to 214165)
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                                                                                                                                                                                                                                                                                         Center project name: zK32I12
                                                                                                                                                                                                                                                                                                                                                                       Center code: SC
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arbitrary. Gaps between the contigs are represented as
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174086. .191682
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85832. .103757
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L47629. .173985
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37778 c 38363 ~
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This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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56136. .80706
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fragment_chain:1"
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fragment_chain:1"
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of 6837 bp in length
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                                                                                                            Rattus ***, 2
                                               AC097421.6 GI:30521335
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED
Rattus norvegicus (Norway rat)
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57; Conserv
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Rattus.
           Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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/note="assembly_fragment:02063.0"
, 38559 c 38612 g 66773 t 211
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fragment_chain:2"
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fragment_chain:3"
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ragment_chain:2"
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             Craniata; Vertebrata; Euteleostomi;
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                                               in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                   Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On May 10, 2003 this sequence version replaced g1:23268037. The sequence in this assembly is a combination of BAC based reads
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Submitted (18-OCT-2001) Human Genome Sequencing
Submitted (18-OCT-2001) Human Genetics, Baylor College
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Baylor Plaza, Houston, TX 77030,
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Rat Genome Sequencing Consortium.
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2 (bases 1
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Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benn
Blswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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Muzny, D. Marie., Metzker, M. Lee., Abramzon, S.,
                                                                                                                                                                                                                                                         and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig descrii
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the ends of the clone and there may be sequence
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                                                                                               RESULT 42
AX702602/c
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LOCUS
DEFINITION
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misc_feature
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114937 ACAGACTTAGAAAGA 114923
                                                                                           114997 AAGTAACTGGATAAAAAATTAATTCAAAATATTAGTAGCTCTCTTATATACAAATGACAA 114938
                                             62 ATACAGTTAAAAAA 76
                                                                                                                                                                                       48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                                                                                                    AAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTA 61
                                                                                                                                                                                                                                                                                                        64169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be preserved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247481
247581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Atlas 3.0;
Consensus quality: 23512 bases at least Q40
Consensus quality: 241068 bases at least Q30
Consensus quality: 242990 bases at least Q20
Estimated insert size: 253299; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center clone name: CH230-24E11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center project name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Baylor Co
Center code: BCM
                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              soon as it is available and the accession number will
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                                                                                                                                                                                                                                                                                                   end_sequence:BH278136"
52992 c 56591 g 70
                                                                                                                                                                                                                                                                                                                                                                                                                  end_sequence:BH278135"
complement(246379...24
                                                                                                                                                                                                                                                                                                                                                     site:EcoRI
                                                                                                                                                                                                                                                                                                                                                                         clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    site:EcoR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5489.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="wgs_end_extension clone_end:T7"
                                                                                                                                                                                                                                                                                                                                                                                              /note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="CH230-24E11"
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                                                                                                                                                                                                          30.9%;
64.0%;
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248948: contig of 1368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247480: contig of 247480 bp in length
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                                                                                                                                                                                    0;
                                                                                                                                                                                                                               Score 31.8;
                                                                                                                                                                                    Mismatches
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bp in length
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                                                                                                                                                                                    27;
                                                                                                                                                                                                                                                                                                     4996 others
                                                                                                                                                                                                                               Length 248948;
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AX702602 Sequence

1604 bp I 188 from Patent WO02059320.

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PAT 03-APR-2003

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AC112392_4 Continuation (3 of 5)
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Continuation (2 of 5)
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AC112392_1/c
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ORIGIN
                                                                                                                                                                                  RESULT 44
AC112392_2/c
                                                                                                                                                                                                                                                                                                                                                                                                                         WPCOMMENT
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                                                                                                                                                                          WPCOMMENT
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                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                   Sequence split into Fragment Name AC112392_0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                  Matches
                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                      Query Match
                                                                                                                                                            Sequence split into
                                                                                                                           AC112392_0
AC112392_1
                                                                                                                                                                                                                                                                                                                                                                         AC112392_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   source
                                                                                                                                                                                                                                                                                                                                                              AC112392_2
                                                                                                                AC112392_
                                                                                                                                                                                                                              102879 ATTACTAGAGCCTGCTTATGTGAACTACCAGAACTCTCAAAGAAACAGTATTTC 102826
                                                                                                                                                                                                                                                                             Local Similarity
les 40; Conserv
                               Local Similarity
les 40; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1130 AAGTGAATGTATTGATATTTTATTTGCAGAAATGAAAGATCTGGCAAAAATGTTTTCCTT 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                32
                                                                                                                                                                                                                                                      32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA sequences of Escherichia coli CFT073
Patent: WO 02059320-A 188 01-AUG-2002;
WISCONSIN ALUMNI RESEARCH FOUNDATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 AAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Blattner, F.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
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AX702602.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
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ATACAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAACA 103
                                Conservative
                                                                                                                                                                                                                                                                               Conservative
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/mol_type="genomic_DNA"
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                                                                                                                                                 Begin
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200001
300001
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                                           30.7%;
74.1%;
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74.1%;
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                              Score 31.6; Di
Pred. No. 65;
O; Mismatches
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210000
310000
410000
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Pred. No. 1.1e+02;
); Mismatches 44;
                                                                                                                                                                                                                                                                                       Score 31.6;
Pred. No. 65
                                                                                                                                                                                                                                                                                                                                                             210000
310000
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                                                                            200001 (AC112392 Rattus norvegicus
                                                    DB 2;
                                                                                                                                                                                                                                                                                                  DB 2; Length 110000;
                               14;
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                               0,
                                                                                                                                                                                                                                                                             0;
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ATTACTAGAGCCTGCTTATGTGAACTACCAGAACTCTCAAAGAAACAGTATTTC

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REFERENCE
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WPCOMMENT
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AC124223_1
AC124223_2
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AC124223
                                                                                                                                                                                                                        Liu, J. Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorensuhewa, L., Loulseged, H., Lozado, R. J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Martin, R., Martinez, E.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E.,
Mangum, B., Mapua, P., Martin, K., Martin, R., Menenen, E.,
Mawhiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Milosavljevic, A., Miner, G., Minja, E., Mentemayor, J., Moore, S.,
Milosavljevic, N., Newton, N., Nguyen, N., Norris, S.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C.,
Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Pluzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D.,
Shetty, J., Shvartsbeyn, A., Sisson, I., Sotelle, R., Sosa, J.,
Valas, R., Vera, V., Villasana, D., Warten, A., Trejos, Z., Usmani, K.,
Wang, O., Wang, S., Warten, J., Warten, R., Wei, X., White, F.,
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     Valas,R., Vera,V., Villasana,D., Waldron,L., Walxel,D., Wung,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F., Williams,G., Willson,R., Wleczyk,R., Wooden,H., Worley,K., Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Wright,R., Bou,J., Zhou,X., Zhao,S., Dunn,D., von Yu,F., Zhang,J., Zhou,J., Zhou,X., Bao,S., Smith,H.O.,
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Biswalo,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
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Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden
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REFERENCE
AUTHORS
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On Oct 12, 2002 this sequence version replaced gi:21465216.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (14-JUN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a 'working draft' sequence. It currently consists of 25 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as
                                                                                                                                                                                                                                                                                                                                                                              as soon as it is available be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                     runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
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                                                                                        /note="wgs_contig"
48484. .51371
/note="wgs_contig"
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44580. .48089
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32433. .41624
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                                                                                                                                                    /note="wgs_contig"
42273. .44529
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26171. .27385
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19740. .26070
                                                                                                                                                                                                                                                                                 clone_end:Sp6
                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                          /note="clone_boundary
                                                                                                                                                                                                                                                                                                                                                   /clone="CH230-486P3"
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400601: contig
400701: gap of
410562: contig
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74.1%;
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y of 5986
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g of 10811 bp in
f unknown length
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g of 3769 bp in lo
f unknown length
g of 63840 bp in
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of 4033
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of 5277
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of 9861 bp in
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Search completed: August 25, 2003, 07:22:02 Job time: 1605 secs

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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
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   US-09-685-853A-3
US-09-801-876B-3
4 US-09-657-884-1
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US-09-453-702B-215
US-09-986-243-106
US-08-991-601-26
US-08-991-601-26
US-08-91-601-1
PCT-US94-00616-1
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PCT-US94-0164-9
US-09-328-352-1715
US-09-328-352-1715
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Sequence 2, Appli
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US-09-685-853A-3/c
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| US-09-996-243-108 | US-09-996-243-104 | US-09-305-839-17 | JS-08-818-655-1 | US-09-054-298-1 | US-08-616-368A-17 | US-09-996-243-105 | US-09-647-826-1 | US-09-107-532A-3072 | US-09-736-457-655 | us-09-702-705-655 | US-09-092-409-52 | US-09-092-409-51 | US-08-680-726A-52 | US-08-680-726A-51 | US-08-473-446-126 | - 80 | US-08-473-446-18 |
| 996- | 996- | 305- | 818- | 054- | 616- | 996- | 647- | 107- | 736- | 702- | 092- | 092- | 580- | -089 | 173 | 113- | 173- |
| 243 | .243 | .839 | 655 | .298 | 368 | 243 | 826 | 532 | 457 | 705 | .409 | 409 | 726 | 726 | 446 | -413-118-126 | 446 |
| -10 | -10 | -17 | -17 | -17 | A-1 | -10 | ۲ | A-3 | -65 | -65 | -52 | -51 | A-5 | A-5 | -12 | -12 | -18 |
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| 108, App | 104, | 17, | 17, | 17, | 17, | 105, | 1, 1 | 3073 | 655, | 655, | 52, | 51, Appl | 52, | 51, | 126, | 126, | 18, |
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ALIGNMENTS

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GENERAL INFORMATION:

APPLICANT: YE, Jane et al

TITLE OF INVENTION: ISOLATED HUMAN KINASE E

TITLE OF INVENTION: ACID MOLECULES ENCODIN-

TITLE OF INVENTION: THEREOF

FILE REFERENCE: CLOO1160

CURRENT APPLICATION NUMBER: US/09/801,876B
                                                                                                                                                RESULT 2
US-09-801-876B-3/c
Sequence 3, Application US/09801876B
Patent No. 6492155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000871
CURRENT APPLICATION NUMBER: US/09/685,853A
CURRENT APPLICATION NUMBER: 205-05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 3
LENGTH: 74962
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/182,194
PRIOR FILING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 3
SOFTMARF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE: misc_feature
NAME/KEY: misc_feature
LOCATION: (1)...(74962)
OTHER INFORMATION: n = A,T,C or
                                                                                                                                                                                                                                                                                                                                                                                                                                                     35.1%;
Local Similarity 62.9%;
nes 56; Conservative
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                                                                                                                                                                                                                                                                                         ANAAAAGGTCTTTCAGTACTTCTCATCTA 63250
                                                ISOLATED HUMAN KINASE PROTEINS, NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES THEREOF
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; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-557-884-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-557-884-1/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09557884
Patent No. 6506581
GENERAL INFORMATION:
APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 55; Conserv
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NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
COMPUTER: Dell Pentium
COMPUTER: COMPM: MS DOS v6.22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73625 AATTGAACAAAGAATTTTGTGCCCTGCTCATTTCTAAC 73588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       73685 TGCATTGCATTATATTGTATAATCACCATTAATATTTTCTTTTTGCCTGAATTGCTCACT 73626
                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scien
STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 CAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAAC 102
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                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/557,884
FILING DATE: 25-Apr-2000
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                        NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB
                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/476,102 FILING DATE: JUN-5-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Rockville
STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA 64
                                                                                                                                               LENGTH: 1830121 base pairs
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28.0%;
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Score 28.8; D
Pred. No. 9.8;
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                DB
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                  4;
                  Length 1830121;
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TOPOLOGY: linear sequence description: seq id no: 1: US-09-643-990A-1
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US-09-643-990A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                              Matches
                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1830121 base pairs
1541171 AAAAATATAATTCCTCTATTCTCATCCA 1541144
                                                                       1541231 ATTAAAGAGTCGTTATTTCCATAATAGTTAGTTGATGTATTATTTCCATTTTCATTTAAT 1541172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1541171 AAAAATATAATTCCTCTATTCTCATCCA 1541144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: 3 1/2 inch diskette

COMPUTER: Dell Pentium

OPERATING SYSTEM: MS DOS v6.22

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/643,990A
FILING DATE: 23-Aug-2000
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human G
                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof; and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                        13 ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                               73 AAAACGGTATTTCCCTGGTTCTGATCCA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73 AAAACGGTATTTCCCTGGTTCTGATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                                                                                                                                              51;
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                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kenley K. Hoover REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 310-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: PB186P1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                            28.0%;
ilarity 58.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mark D. Adam
Owen White
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Craig Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hamilton O. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09643990A
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                                                                                                                                            Score 28.8; DB Pred. No. 9.8; 0; Mismatches
                                                                                                                                              0;
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                                                                                                                                                                               DB 4;
                                                                                                                                              37;
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                                                                                                                                                                               Length 1830121;
                                                                                                                                              Indels
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                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                 Sequence 106, Application US/09996243 Patent No. 6478825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local (
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Patent No. 6365723
GENERAL INFORMATION:
APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                       APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
   APPLICANT:
                                      PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (608) 251-91 INFORMATION FOR SEQ ID NO: 215:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-1998
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27386
REGERENCE/DOCKET NUMBER: 960296.
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible operating SYSTEM: PC-DOS/MS-DOS SOFTMARE: Word Perfect 8.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: 1 South Pinckney Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 215:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR
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MEDIUM TYPE: Diskette, 3.50 inch.
                                                                                                                                                                                                                                                                                                                                                                                                   1069. TTTTGGACAATATAAAACACTTATCGAAGATCTGATTGAACA 1028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1129 ACGTGAATGCACTGATATTTTATTTGCAGAAATGAAAGAACTAGCAAAAATGTTTTCCTT 1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              62 ATACAGTTAAAAAAACGGTATTTCCCTGGTTCTGATCCAACA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 AAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTA 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2692
TYPE: nucleic acid
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FILING DATE: 03-Dec-1999
CLASSIFICATION: <UNknown>
RAPPLICATION DATA:
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STATE: WI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OF SEQUENCES:
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Plunkett, e.,
Physical Properties
Permanents
Per
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28.4;
Pred No. 2.
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-02
                                                                                          APPLICATION NUMBER: 60/
FILING DATE: 1998-06-05
                                                                                                                                                           APPLICATION NUMBER: 60/088326 FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 1998-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/
FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 60/087827
FILING DATE: 1998-06-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
APPLICATION NUMBER: 60/087607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                        APPLICATION NUMBER: 60/
FILING DATE: 1998-06-05
                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                         FILING DATE: 1998-06 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/088026 FILING DATE: 1998-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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1998-05-07 1998-04-28

60/084600

1998-06-04 1998-06-04 1998-06-04

60/088025 60/088021 60/087759 60/087609

.998-06-04

60/088033 60/088030 60/088029 60/088028

60/088202

60/088167

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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
                                                                                                                                                                                                                                                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
FILE REFERENCE: P2730P1C13
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FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/083322
                                                            FILING DATE: 1998-02-25
                                                                                APPLICATION NUMBER:
                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kljavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gurney, Austin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Godowski, Paul
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ferrara, Napoleone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumas, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Paoni, Nicholas F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Napier, Mary A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Grimaldi,J.Christopher
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art, Timothy A.
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OR FILING DATE: 1998-06-16
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OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089538
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089598
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R FILLING DATE: 1998-06-17
N APPLICATION NUMBER: 60/089653
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OR APPLICATION NUMBER: 60/089801
R FILLING DATE: 1998-06-18
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DR FILING DATE: 1998-06-10
DR APPLICATION NUMBER: 60/088742
DR FILING DATE: 1998-06-10
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/088876
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FILING DATE: 1998-06-10
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FILING DATE: 1998-06-12
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RESULT 7
US-08-981-601-26/c
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                                                                               Sequence 26, Applicati
Patent No. 6133023
GENERAL INFORMATION:
APPLICANT: MADSEN,
APPLICANT: VRANG,
APPLICANT: VRANG,
APPLICANT: ARNAU,
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R FILING DATE: 1998-06-26

DR APPLICATION NUMBER: 60/091360

DR FILING DATE: 1998-07-01

DR APPLICATION NUMBER: 60/091478

DR FILING DATE: 1998-07-02

DR APPLICATION NUMBER: 60/091544

DR APPLICATION NUMBER: 60/091519

DR APPLICATION NUMBER: 60/091519
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DR FILING DATE: 1998-06-25
DR APPLICATION NUMBER: 60/990696
DR FILING DATE: 1998-06-25
DR APPLICATION NUMBER: 60/990862
DR FILING DATE: 1998-06-26
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APPLICATION NUMBER: 60/091978
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FILING DATE: 1998-06-24
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156 CCCTGTAAAAAATAGTA 140
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OF INVENTION:
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5. 6133023
                                                                                                                                                                                                                                                                               65 CAGTTAAAAAAACGGTA 81
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46; Conserv
            GROENVALD JOHNSEN, MADS
ISRAELSEN, HANS
JERTION: A LACTIC ACID BACTERIAL REGULATABLE
                                                              MADSEN, Soeren Michael
VRANG, Astrid
ARNAU, Jose
RAVN, Peter
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Best Local Similarity
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                               TITLE OF INVENTION: TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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                                            COUNTRY:
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                                                                     E: Foley & Lardner
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06-SEP-1996
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n Release #1.0, Version #1.30
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                                                                                                                                                              Recombinant · Lactic Acid Bacterium
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Best Local Similarity
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NUMBER OF SEQUENCES:
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                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
TELEPHONE: (617) 876-1170 x8574
                             NAME: Meinert, Maureen C.
REGISTRATION NUMBER: 31,544
REFERENCE/DOCKET NUMBER: GI
                                                                                                                                                                   COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                STATE:
                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: BENT, Stephen A REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 25-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                         APPLICATION NUMBER: FILING DATE: 23-FE
                                                                                                                                                       SOFTWARE:
                                                                                                                                                                                                                                               COUNTRY:
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                                                                                                                                                       PatentIn
                                                                                                                                                                E: Floppy disk
IBM PC compatible
SYSTEM: PC DOS/MS-DOS
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                                                                                                                                                     Release #1.0, Version #1.25 (EPO)
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                                 GI 5201-FWC
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Pred. No. 4;
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                                                                                                                                                                                                                                                                                                          Inc. - Legal Affairs
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RESULT 11
US-09-484-970B-138
; Sequence 138, Application US/09484970B
; Patent No. 6426186
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                                                                                                GENERAL INFORMATION:
APPLICANT: Jones,
APPLICANT: Volkmut
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
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                                               APPLICANT: Walker, michael G.
TITLE OF INVENTION: BONE REMODELING GENES
FILE REFERENCE: PB-0014 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2581 base pair
                CURRENT APPLICATION NUMBER: US/09/484,970B
CURRENT FILING DATE: 2000-01-18
   NUMBER OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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MOLECULE TYPE:
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STRANDEDNESS: single
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
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                                                                                              Jones, Karen A.
Volkmuth, Wayne
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 ID NOS:
                                                                                                                                                                                                                                                                                                                                                                             Conservative
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2000-01-18
172
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55.1%;
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Pred. No. 5;
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; OTHER INFORMATION: Incyte ID No.'6426186 336987.1CB1
US-09-484-970B-138
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                                                                                                                                                                                                                                                                 SEQ ID NO 196
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SEQ ID NO 138
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PRIOR APPLICATION NUMBER: US 60/131,971
PRIOR FILING DATE: 1999-04-30
PRIOR APPLICATION NUMBER: US 60/132,065
PRIOR FILING DATE: 1999-04-30
                                                                                                                                                                                                                                                                                   SOFTWARE:
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                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-07-29
PRIOR APPLICATION NUMBER: US 60/146,452
PRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/145,915 PRIOR FILING DATE: 1999-07-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/539,333D CURRENT FILING DATE: .2000-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Essioux, Laurent
TITLE OF INVENTION: SCHIZOPHENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
FILE REFERENCE: GENSET.047AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 1999-10-28 PRIOR APPLICATION NUMBER: US
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TYPE: DNA
                                     FEATURE:
                                                     OTHER INFORMATION: 99-26228-172.mis1
                                                                      NAME/KEY: misc_binding LOCATION: 1482..1500
                                                                                                                FEATURE:
                                                                                                                             OTHER INFORMATION: 99-26228-172 : polymorphic base
                                                                                                                                                 NAME/KEY: allele
LOCATION: 1501
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                          ORGANISM: Homo Sapiens
                                                                                                                                                                                                                              TYPE: DNA
 COCATION:
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51; Conserv
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56.7%;
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Pred. No. 5
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RESULT 14
US-09-410-464-9
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US-09-220-132-2
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GENERAL INFORMATION:
APPLICANT: Strauss et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation
TITLE OF INVENTION: poplar and other plant species.
FILE REFERENCE: 53375
                                                                                            Sequence 9, Application US/09410464 Patent No. 6395892
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 2
LENGTH: 5508
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Patent No. 6506607
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Best Local Similarity
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CURRENT FILING DATE: 1998-12-23
PRIOR APPLICATION NUMBER: US 60/079,303
PRIOR FILING DATE: 1998-03-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND ASSESSMENT
TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANCE
FILE REFERENCE: 07334-074001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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TYPE: DNA
ORGANISM: Homo sapiens
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LOCATION: 1489..1513
OTHER INFORMATION: 99-26228-172
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LOCATION: 1330..1350
OTHER INFORMATION: upstream
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Pred. No. 6;
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Pred. No. 6.9;
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US-09-328-352-1715/c
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US-09-734-674-3/c
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                                                    ; GENERAL INFORMATION:
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APPLICANT: WEI, MING-Hui et al
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUM
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CLOO1018
CURRENT APPLICATION NUMBER: US/09/734,674
CURRENT FILING DATE: 2000-12-13
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SEQ ID NO 9
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Best Local
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CURRENT FILLING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER FILING DATE: 1999-04-06
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 60/
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
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ORGANISM: Human
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Pred. No. 17;
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FILE REFERENCE: GTC99-03PA

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; ORGANISM: Ureaplasma urealyticum
US-09-601-198-108
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-1715
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APPLICANT: Chen, Ellson Y.
APPLICANT: Glass, Jennifer S.
APPLICANT: Glass, John I.
APPLICANT: Heiner, Cheryl R.
APPLICANT: Lefkowitz, Elliot
                                                                                                                                          Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/073,189
PRIOR FILING DATE: 1998-01-30
NUMBER OF SEQ ID NOS: 181
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 108
LENGTH: 3255
                                                                                                                             Patent No. 6100449
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Best Local Similarity
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SEQ ID NO 1715
LENGTH: 306
                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/601,198
CURRENT FILING DATE: 2000-12-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA TITLE OF INVENTION: UREALYTICUM FILE REFERENCE: UAB-13452/22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04
      TITLE
                                    APPLICANT:
                                                 APPLICANT:
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                                                                                              APPLICANT: FLUHR,
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    OF INVENTION: A GENE
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                              ORI, Naomi
PARAN, Ilan
ZAMIR, Daniel
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Pred. No. 7
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Pred. No. 4;
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   TRANSFORMATION
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US-09-328-352-1417
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US-09-328-352-1417
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: GATY L. BICTON et al.
APPLICANT: GATY L. BICTON et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
                                                                                                                                                                               NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 1417
                                                            Matches
                                                                           Best
                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                   Sequence 1417, App
Patent No. 6562958
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/328,352 CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                 TYPE: DNA
                                                                                                                                                                  ENGTH: 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 113,373
FILING DATE: 13-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/05272
FILING DATE: 15-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 09-DEC-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
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                                                                         Local
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                         2742 TCCAAACAAGGGAGTTGTCCTAGTGCTG 2715
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548 GTTTATTGGCAGCATTTTTAGTTTTTGCTTTTCTTATTTTTGTTAGACGTAAATTGTGACT 607
                  83
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                                                                           Similarity
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ucleic acid
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                                                           Conservative
                                                                                                                                                                                                                                                                                                                                Application US/09328352
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                                                                         Score 27;
Pred. No.
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Pred. No. 7
                                                           Mismatches
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                                                                                       Length 1287;
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                                                           Indels
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                                                         Gaps
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608 ATATTGCACTGGGTC

622 93

GTATTTCCCTGGTTC

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; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-356-952-11
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US-09-356-952-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 10, Application US/09791211 Patent No. 6448080 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                   SEQ ID NO 10
LENGTH: 98844
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LENGTH: 5398
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Best Local
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APPLICANT: Andrew T. Watt
TITLE OF INVENTION: ANTIS
FILE REFERENCE: RTS-0205
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EARLIER APPLICATION NUMBER: 60/093,631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILE REFERENCE: 600-1-228N CURRENT APPLICATION NUMBER: US/09/356,952
                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/791,211
CURRENT FILING DATE: 2001-02-23
NUMBER OF SEQ ID NOS: 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: CO1e, Philip
APPLICANT: Kuriyan, John
TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Margarit, S. M. APPLICANT: Bor-Sogi, Dafna
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Boriack-Sjodin,
                                                                                                                                 NAME/KEY: unsure LOCATION: 64383
                                                                                                                                                                       OTHER INFORMATION: unknown
                                                                                                                                                                                       NAME/KEY: unsure LOCATION: 24962
                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo sapiens
                                                       OTHER INFORMATION:
                                                                                                               OTHER INFORMATION:
                     NAME/KEY: unsure LOCATION: 65469
                                                                                         NAME/KEY: unsure
                                                                           OCATION: 65468
INFORMATION: unknown
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52; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                      Andrew T. Watt
WENTION: ANTISENSE MODULATION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                       unknown
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Pred. No. 1
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**COPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: US-09-557-884-1
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US-09-557-884-1
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Best Local Similarity
                                     Query Match
Best Local 9
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SEQUENCE CHARACTERISTICS:
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OTHER INFORMATION:
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   Local Similarity 64.1 hes 40; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Michelle S. Marks
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB18
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
TELEFAX: 301-309-8439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78668 TTAAGAGCTCATAAATGTACTCATTGCTAATATATTTAATGAAATGTTAATTGC 78615
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COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences,
STREET: 9410 Key West Avenue
CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Fleischmann et al.
TITLE OF INVENTION: The Nucleotide sequence of
the Haemophilus influenzae Rd Genome, Fragments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/557,884 FILING DATE: 25-Apr-2000 CLASSIFICATION: <Unknown>
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COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
SOFTWARE: ASCII Text
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/09557884
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                                                                                                                                                                                                                    TOPOLOGY: linear
                                                                                                                                                                                                                                                                                TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 08/476,102 FILING DATE: JUN-5-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: MD
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                                                                                                                                                                                                                                                                                                                     LENGTH: 1830121 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1/2 inch diskette
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Score 26.8; D
Pred. No. 40;
0; Mismatches
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Pred. No. 22;
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                                                                          DB 4;
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                                                                   Length 1830121;
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                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Applicatio Patent No. 6528289 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                   TELEPHONE: 301-610-57:
TELEPAX: 310-309-8439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
1819527 AA 1819528
                                                            1819467 AAAATAGCTTAATCACTACCTTAATACTTTATTAATTTGTCTTTTTCTAATTTACTTAAC 1819526
                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/487,429
FILING DATE: 1995-06-07
APPLICATION NUMBER: 08/426,787
FILING DATE: 1995-04-21
ATTORNEY/AGENT INFORMATION:
NAME: Kenley K. HOOVET
REGISTRATION NUMBER: 40,302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1819527 AA 1819528
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CLASSIFICATION DATA:

APPLICATION NUMBER: US/09/643,990A.

FILING DATE: 23-Aug-2000

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 301-610-5790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 inch diskette
                                                                                                                                                                                                                                SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Scients STREET: 9410 Key West Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                               13 ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                                  73 AA
                                                                                                                                           40;
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                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: Dell Pentium
OPERATING SYSTEM: MS DOS v6.22
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                                                                                                                                                                                                                                                                                                  LENGTH: 1830121 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Application US/09643990A
                                  74
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INVENTION: The Nucleotide sequence of the Haemophilus influenzae Rd Genome, Fragments Thereof, and Uses Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Robert D. Fleischmann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamilton O. Smith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Owen White
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                                                                                                                                                        26.0%;
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                                                                                                                                                        Score 26.8;
Pred. No. 40;
                                                                                                                                      Mismatches
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                                                                                                                                                                         Length 1830121;
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US-09-092-409-53/c
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US-08-680-726A-53/c
                                                                                                                                                     Sequence 53, Application US/09092409 Patent No. 6159478 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (303) 863-022
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                  APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
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CORRESPONDENCE ADDRESS:
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STREET: 1. STREET: 2. Colora
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                 STATE:
                               CITY:
                                          STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: FILING DATE: 12-JUJ CLASSIFICATION: 42
COUNTRY:
                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 11
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Connell, Gary J
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                        640 AAAAAAGTTCATCGTCAACTTTTGATGCTCCTACAGATCTAGATTCCTTACACCATTCCA 581
                                                                                                                                                                                                                                                              580 TAAAAGTTGGTTC
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5804197
                              Denver
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               Colorado
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                                          1700 Lincoln Street, Suite 3500
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U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                            Sheridan Ross & McIntosh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Elizabeth J.
                                                                                                                                                                                                                                                                                                                                                                                                  25.8%;
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Pred. No. 8.4;
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COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                             COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN RCLEASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESSE: Curtis, Morris & Safford
STREET: 530 Fifth Avenue
                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                APPLICANT: Limbach, TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                CLASSIFICATION:
                                                          APPLICATION NUMBER: US/0 FILING DATE: 30-MAR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                             CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Connell, Gary J
REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
REGISTRATION NUMBER:
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                                                                             US/08/220,151
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Pred. No. 8.4;
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                                                                                                              Version #1.25
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Patent No.
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                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08,
FILING DATE: 30-MAR-1994
ATTORNEY/AGENT INFORMATION:
NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,50
TOPOLOGY: 1
                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 1320 base pairs
                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: PAOLETTI, ENZO APPLICANT: LIMBACH, KEITH
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: NEW YORK
STATE: NEW YORK
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                            STRANDEDNESS:
                                                                                                                                                   REFERENCE/DOCKET NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE: 29-MAR
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TYPE: nucleic acid
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                                                                                                                      CELEPHONE:
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                                                                                                     E: (212) 840-3333
(212) 840-077
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(212) 840-0712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LIMBACH,
                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
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Pred. No. 8
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Score 26.6;

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Length 1320;

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Sequence 126, Application US/08413118
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Best Local
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Matches 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                     MOLECULE TYPE:
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NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: CURTIS, MORRIS
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
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ZIP: 10036
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DEDNESS: single
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                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAOLETTI,
                                                                                                                                                                                                                                                                                                                                                                                      (212) 840-3333
                                                                                                                                                                                                          25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEOTIDE AND AMINO ACID SEQUENCES OF CANINE HERPESVIRUS 9B, 9C, AND 9D AND USES THEREFOR
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                                                                                                                                                                                                          Score 26.6; D. Pred. No. 8.9;
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US-08-473-446-126/c
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                                                                                                                                                                                                     GENERAL INFORMATION:
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                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: CURTIS, M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 25,506
REFERENCE/DOCKET NUMBER: 45
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 840-333
                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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CURRENT APPLICATION DATA:
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ADDRESSEE: CURTIS, M
COMPUTER READABLE FORM
                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                      FITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PAOLETTI, APPLICANT: LIMBACH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
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                                             STATE:
                                                                           STREET:
                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: NEW YORK
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                            939 AAAAAAGTTCATCGTCAACTTTTGATGCTCCTACAGATCTAGATTCCTTACACCATTCCA
                                                                                                                                                                                                                                                                                                                879 TAAAAGTTGGTTC 867
                                                                                                                                                                                                                                                                                                                                             73 AAAACGGTATTTC 85
                                                                                                                                                                                                                                                                                                                                                                                                     13 ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
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              10036
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                          NEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FROMMER, WILLIAM S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleic acid
                                          NEW YORK
                                                                       E: CURTIS, MORRIS & SAFFORD, 530 FIFTH AVENUE, 25TH FLOOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1415 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 530 FIFTH AVENUE,
                           UNITED STATES OF AMERICA
                                                                                                                                                                     LIMBACH,
                                                                                                                                                                                  PAOLETTI, ENZO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PAOLETTI, ENZO
                                                          YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IBM PC compatible
SYSTEM: PC-DOS/MS-DOS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                    NUCLEOTIDE AND AMINO ACID SEQUENCES OF CANINE HERPESVIRUS gB, gC, AND gD AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25.8%;
                                                                                                                                                                      KEITH J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUCLEOTIDE AND AMINO ACID SEQUENCES CANINE HERPESVIRUS 9B, 9C, AND 9D AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEITH J.
                                                                                                                        128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MORRIS & SAFFORD, P.C. AVENUE, 25TH FLOOR
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Pred. No. 9.1;
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                                                                                                                                    AND GD AND USES THEREFOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1415;
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SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:

MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

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RESULT 31
US-08-680-726A-51/c
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US-08-473-446-126
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                                                                   APPLICATION NUMBER: US/08/680
FILING DATE: 12-UU-1996.
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
TELEFAX: (303)
NFORMATION FOR SEQ
                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES NUMBER OF SEQUENCES: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: FROMMER, WILLIAM S.
REGISTRATION NUMBER: 25,506
REFERENCE, DOCKET NUMBER: 454310-2670
TELECOMMUNICATION INFORMATION:
                                  TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Haanes, Elizabeth J.
                                                                                                                                                                                                                                                                                                                                                      STREET: 1700 | CITY: Denver | STATE: Colora:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 25.8%;
Local Similarity 60.3%;
les 44; Conservative
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                                                                                                                                                                                                                                                                                                                                                    Colorado
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1700 Lincoln Street, Suite 3500
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                 863-0223
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                                                                         2618-46-C1
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US-08-680-726A-52
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Best Local Similarity
                                                                                                                       Matches
                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                            TELEFAX: (303) 863-022
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 10592 base pai
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MOLECULE TYPE:
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                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                  STRANDEDNESS: Si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                  TYPE:
                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                     NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 12
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/680,726A FILING DATE: 12-JUL-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Denver
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                                                                                                                                       Local Similarity
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                                                          4826 AAAAAAGTTCATCGTCAACTTTTGATGCTCCTACAGATCTAGATTCCTTACACCATTCCA 4885
                           73 AAAACGGTATTTC
                                                                                       13 ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 AAAACGGTATTTC 85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     44; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1700 Lincoln Street, Suite 3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.A.
                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Haanes, Elizabeth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheridan Ross & McIntosh
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                                                                                                                                      25.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RECOMBINANT CANINE HERPESVIRUSES
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60.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
4898
                                                                                                                                                                                                                                                                                             52:
                                                                                                                       0;
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                                                                                                                                    Score 26.6;
Pred. No. 15
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Pred. No. 15;
                                                                                                                       Mismatches
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US-09-092-409-52
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; MOLECULE TYPE:
US-09-092-409-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFRICE: (303) 863-0223
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10592 base pairs
TYPE: nucleic acid
                                                                                                                                                                   Sequence 52, Application US/09092409 Patent No. 6159478
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                 CORRESPONDENCE ADDRESS:
                                                                                  TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                APPLICANT: Haanes, Elizabeth J. APPLICANT: Frank, Rexann S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Haanes, Elizabeth J.
APPLICANT: Frank, Rexann S.
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES
NUMBER OF SEQUENCES: 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Denver
STATE: Colora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/81
                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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                                                                                                                                                                                                                                                                           5707
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                                                                                                                                                                                                                                                                                            73 AAAACGGTATTTC 85
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               Denver
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Colorado
                               1700 Lincoln Street, Suite 3500
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                                               Sheridan Ross & McIntosh
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                                                                                                  RECOMBINANT CANINE HERPESVIRUSES
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Pred. No. 15;
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 Length 10592;

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US-09-702-705-655/c
                                                              US-09-702-705-655
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                                                                                         SOFTWARE: Fa
SEQ ID NO 655
LENGTH: 494
TYPE: DNA
Query Match
Best Local Similarity
Matches 39; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 655,
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                                                                                                                                                                                                 TITLE OF INVENTION: COMPOSITIONS AND METHODS TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER FILE REFERENCE: 210121.478C14
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/702,705
CURRENT FILING DATE: 2000-10-30
NUMBER OF SEQ ID NOS: 1833
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                                                                           ORGANISM: Homo sapien
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REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-JUL-1996
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Rel
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                                                                                                                                       FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                            Carter, Darrick
Retter, Marc
Mannion, Jane
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Lodes, Michael A.
Fanger, Gary
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              25.6%;
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              Score 26.4;
Pred. No. 8.
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Pred. No. 15;
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                              DB 4;
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                                                                                                                                                                                                                                 FOR THE THERAPY AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                              Length 494;
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Indels
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0;
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Gaps
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0;
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RESULT 37
US-09-107-532A-3072
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; ORGANISM: Homo sapien
US-09-736-457-655
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US-09-736-457-655/c
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Sequence 3072, Application.

Patent No. 6583275

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: NOCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION:

CONTROL OF CON
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LENGTH: 494
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 39; Conserv
                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
ATTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 AAGTGAATTTTATGATAGCTACATAAAGGAATTAAGAGCTCCTGCAGAGTTCCTTTGCGA 81
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                      APPLICATION NUMBER: 60/085,598 FILING DATE: 14 May 1998 APPLICATION NUMBER: 60/051571 FILING DATE: July 2, 1997
                                                                                                                                                                                                                                   COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
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                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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Retter, Marc
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Vedvick, Tom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mannion, Jane
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                         ; Sequence 105, Appl
; Patent No. 6478825
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APPLICANT: Nicklin, Martin
APPLICANT: Nicklin, Martin
APPLICANT: Interleukin Genetics, Inc.
TITLE OF INVENTION: TRANSGENIC MODELS OF INF
FILE REFERENCE: MSA-003.01
CURRENT APPLICATION NUMBER: US/09/647,826
CURRENT FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: GB 9723835.6
PRIOR FILING DATE: 1997-11-13
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                                                                                              US-09-996-243-105/c
                                                                                                                            RESULT 39
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-647-826-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 38
US-09-647-826-1
                      GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09647826 Patent No. 6437216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 3072:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 6350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: circular MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 1293 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       5216 GGATTAGATGCTCCTGCATTTGTGAAATGGTTATAAGCATAGAAAAA 5262
                      INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   573 TAAGAAAGAATTGAAAGAAGTAGAAGCTCATCGAGAGCGCAATCGCCAAAAAAAGAAAAAA 632
                                                                                                                                                                                                                                     30 GCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAAAAAA 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 TAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAAA 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 AAACGGTATTTCCCTGGTT 92
                                                                                                                                                                                                                                                                                                                34;
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                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Ariniello, Pamela REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: GTC-012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Enterococcus faecium
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                                                                          Application
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72.3%;
                                                                          US/09996243
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Pred. No. 18;
0; Mismatches
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Pred. No. 12;
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APPLICANT: Napler, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Pan, James
APPLICANT: Panni, Nicholas F.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/96,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-16
PRIOR ETLING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065116
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-02-25
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R FILING DATE: 1998-06-02

DR APPLICATION NUMBER: 60/087759

DR FILING DATE: 1998-06-02

DR APPLICATION NUMBER: 60/087827

DR FILING DATE: 1998-06-03
                                                            R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/01
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/01
R FILING DATE: 1998-06-04
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R APPLICATION NUMBER: 60/01
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APPLICATION NUMBER: 60/
FILING DATE: 1998-05-07
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FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
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Botstein, David
Desnoyers, Luc
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Godowski, Paul J.
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E: 1998-06-04
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OR APPLICATION NUMBER: 60/089514
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089538
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089598
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089599
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089599
OR FILING DATE: 1998-06-17 OR APPLICATION NUMBER: 60/088861
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088876
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089440
OR APPLICATION NUMBER: 60/089410
OR APPLICATION NUMBER: 60/089512 R FILING DATE: 1998-06-R APPLICATION NUMBER: (R FILING DATE: 1998-06-R APPLICATION NUMBER: (DR FILING DATE: 1998-06-10

PR FPLICATION NUMBER: 60/088824

DR FILING DATE: 1998-06-10

PR APPLICATION NUMBER: 60/088826

DR FILING DATE: 1998-06-10

PR APPLICATION NUMBER: 60/088858

PR FILING DATE: 1998-06-11 R FILING DATE: 1998-06
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R FILING DATE: 1998-06 FILING DATE:
APPLICATION 1 FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089952
FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090254 FILING DATE: 1998-06-22 FILING DATE: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 FILING DATE: 1998-06-10
APPLICATION UMBER: 60/088742
FILING DATE: 1998-06-10
APPLICATION UMBER: 60/088810 FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-10 APPLICATION NUMBER: APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: NUMBER: 1998-06-23 1998-06-22 1998-06-22 1998-06-17 1998-06-24 1998-06-23 1998-06-18 1998-06-18 1998-06-05 1998-06-05 998-06-05 60/090429 60/090355 60/090349 60/090252 60/089947 60/089653 60/090431 60/090246 60/089908 60/088738 60/088734 60/088655 60/088212 60/088202

APPLICATION NUMBER: 60/090435

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RESULT 40
US-08-616-368A-17/c
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Best Local
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                                                                           GENERAL INFORMATION:
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FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/092182
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APPLICATION NUMBER: 60/
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                                                                                                                                                                                122 GCCTGTAAAAAATANTA 106
                                                                                                                                                                                                                                        182 TGANTGGTTGAAATCTTTCATGGTGGGATAAATAACANCTGCATCTATGATAATCCACCA 123
                                                                                                                                                                                                                                                                                                                  Similarity
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Lee, Murther Haber, Edgar Haber, Mukesh Yet, Shaw-Fang
                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                 Score 26; DB
Pred. No. 11;
0; Mismatches
                                                                                                                                                                                                                                                                                                                             DB 4; Length 490;
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RESULT 41
US-09-054-298-17/c
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                                                                                                                                                                                                                                                                                 Patent No. 6136953
GENERAL INFORMATION:
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                                                                                                                                                                                              APPLICANT: Lee, Mu-En
APPLICANT: Haber, Edg
APPLICANT: Jain, Muke
APPLICANT: Yet, Shaw-
TITLE OF INVENTION: S
NUMBER OF SEQUENCES:
                                                               COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
           OPERATING SYSTEM: Windows 95
SOFTWARE: FastSEQ for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
TELECOMMUNICATION INFORMATION:
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: fish & Richardson P.C.
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Ri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
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NUMBER OF SEQUENCES:
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TELEFAX: 200154
                                                                                                                                        STREET:
CITY: E
                                                                                                                                           ADDRESSEE: FISH a NECESTREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish Correct 225 Franklin Street
                                     COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                            STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
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APPLICATION NUMBER:
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                                                                                                                                                                         Haber, Edgar
Jain, Mukesh
Yet, Shaw-Fang
Ter, Show-Fang MUSCLE CELL LIM PROTEIN
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SYSTEM: PC-DOS/MS-DOS
                                                    IBM Compatible
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63.9%;
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                                                                                                                                                                    Richardson P.C
US/09/054,298
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Pred. No. 11;
0; Mismatches
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                            Version
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US-08-818-655-17/c
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               INFORMATION FOR SEQ
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SEQUENCE CHARACTERISTICS:
LENGTH: 297 base pairs
SEQUENCE CHARACTERISTICS:
                                                      TELECOMMUNICATION INFORMATION:
                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/61
FILING DATE: 15-MAR-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: SMOOTH MUSCLE CELL LIM PROTEIN NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
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                                                                    NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 05
                                                                                                                                                                                                                                          COMPUTER: IBM CON
OPERATING SYSTEM:
                            TELEFAX:
                                                                                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 02110-2804
                                                                                                                                                                                     APPLICATION NUMBER: US/08/818,655 FILING DATE: 14-MAR-1997
                                        TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
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REGISTRATION NUMBER: P-42,306
REFERENCE/DOCKET NUMBER: 05433/022002
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                           617-542-8906
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Jain, Mukesh
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                                        617-542-5070
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               ID NO:
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Pred. No. 11;
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; TYPE: DNA
; ORGANISM: Murinae gen. sp.
US-09-305-839-17
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US-09-305-839-17/c
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                                                                                                                                                                                                                         Sequence 104, Application US/09996243 Patent No. 6478825
                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 17
LENGTH: 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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APPLICANT: Yet, Shaw-Fang
TITLE OF INVENTION: Methods of Treating Hypertension
FILE REFERENCE: 21508-064
CURRENT APPLICATION NUMBER: US/09/305,839
CURRENT FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: 08/818,655
PRIOR FILING DATE: 1997-03-14
NUMBER OF SEQ ID NOS: 46
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   APPLICANT:
                APPLICANT:
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TOPOLOGY: lin
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39; Conserv
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                                                                                   Fong, Sherman
Gerber, Hanspeter
Kljavin, Ivar J
               Gurney,Austin L.
                            Grimaldi,J.Christopher
                                                        Goddard, Audrey
                                                                                                                 Ferrara, Napoleone
                                                                                                                                 Eaton, Dan L.
                                                                                                                                                            Botstein, David
                                                                                                                                                                           Baker, Kevin P
                                            Godowski,Paul J.
                                                                       Gerritsen, Mary E.
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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APPLICATION NUMBER: 60/
FILING DATE: 1998-02-25
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stewart, Timothy A.
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DR APPLICATION NUMBER: 60/089948
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DR APPLICATION NUMBER: 60/089952
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DR APPLICATION NUMBER: 60/090246
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APPLICATION NUMBER: 60/090431
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APPLICANT: AShkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: "-----in. David
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OR APPLICATION NUMBER: 60/091360

OR FILLING DATE: 1998-07-01

OR APPLICATION NUMBER: 60/091478

OR FILLING DATE: 1998-07-02
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APPLICATION NUMBER: 60/091626
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                                          Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Kljavin, Ivar J.
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                                                                                                                            Gerber, Hanspeter
Gerritsen, Mary E.
                                                                                                                                                                                                              Desnoyers,Luc
                                                                                                                                                                Fong, Sherman
                                                                                                                                                                               Ferrara, Napoleone
Paoni, Nicholas
                             Napier, Mary A.
                                                                                                                                                                                                Eaton, Dan L.
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0; Mismatches
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Pred. No. 13;
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088028
OR APPLICATION NUMBER: 60/088029
OR APPLICATION NUMBER: 60/088029
OR FILING DATE: 1998-06-04
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OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
OR FILING DATE: 1998-03-20
OR APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
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APPLICATION
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APPLICATION NUMBER: 60/088326
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-03
APPLICATION NUMBER: 60/088021
FILING DATE: 1998-06-04
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FILING DATE: 1998-06-02
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FILING DATE: 1997-10-17
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FILING DATE: 1997-11-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Williams, P. Mickey
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art, Timothy
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FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/090246
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DR FILING DATE: 1998-07-01
DR APPLICATION NUMBER: 60/091478
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DR FILING DATE: 1998-07-02
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FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/090696
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APPLICATION NUMBER: 60/090678
222 GCCTGTAAAAAATAGTA
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                                           65 CAGTTAAAAAAACGGTA 81
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45; Conservative
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Search completed: August 25, 2003, 07:50:31 Job time: 52 secs

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Maximum Match 100%
Listing first 45 summaries
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seq length: 2000000000
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2003 Compugen Ltd
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/cgn2_6/ptcodata/2/pubpna/PCT_NEW_PUB.seq:*
/cgn2_6/ptcodata/2/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptcodata/2/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptcodata/2/pubpna/USO7_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US09.NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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                                                 US-10-109-551-3

US-10-027-632-320680

US-10-027-632-79603

US-09-801-876B-3

US-09-801-876B-3

US-10-254-869-3

US-10-27-632-11949
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                  US-10-114-170-215
US-09-989-722-106
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US-10-027-632-230735

US-10-027-632-202236

US-10-027-632-202237
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1852.487 Million cell updates/sec
Sequence 1, Appli
Sequence 215, App
Sequence 106, App
Sequence 106, App
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Sequence 3, Appli
Sequence 3, Appli
Sequence 320680,
Sequence 79603, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 11949, A
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Sequence
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230735,
202236,
202237,
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ALIGNMENTS

US-10-274-974-3/c

Sequence 3, Application US/10274974 Publication No. US20030054490A1 GENERAL INFORMATION:

ENCODING HUMAN PHOSPHATASE PROTEINS,

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; NAME/KEY: misc_feature
; LOCATION: (1)...(74962)
; OTHER INFORMATION: n =
US-10-274-974-3
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                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Wi
SEQ ID NO 3
LENGTH: 74962
TYPE: DNA
ORGANISM: Homo sapien
                                                                                                                                           Matches
                                                                                                                                                        Query Match
Best Local :
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PRIOR FILING DATE: 2000-10-11
PRIOR APPLICATION NUMBER: 60/182,194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: WEI, Ming-Hui et al.
TITLE OF INVENTION: ISOLATED HUMAN PHOSPHATASE PROTEINS,
TITLE OF INVENTION: NUCLECIC ACID MOLECULES ENCODING HUD
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: CL000871 DIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/274,974 CURRENT FILING DATE: 2002-10-18
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                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                  FEATURE:
63278 AAAAAAGGTCTTTCAGTACTTCTCATCTA 63250
                                                                     72 AAAAACGGTATTTCCCTGGTTCTGATCCA 100
                                                                                         12 AATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAA 71
                                                                                                                                           56;
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                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                       for Windows Version 4.0
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                                                                                                                                                        Score 36.2; DB Pred. No. 0.89;
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                                                                                                                                          Mismatches
                                                                                                                                                                         DB 14;
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; ORGANISM: Human
US-10-027-632-230735
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US-10-027-632-230735/c
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 230735
LENGTH: 585
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PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
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PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
                                               PRIOR APPLICATION NUMBER: US 60/146,002 PRIOR FILING DATE: 1999-08-09
                                                                                             PRIOR APPLICATION NUMBER: US PRIOR FILING DATE: 1999-09-28
                                                                                                                                            PRIOR APPLICATION NUMBER: US 60/167,363 PRIOR FILING DATE: 1999-11-23
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PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/198,676
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56; Conserv
FastSEQ
                         SEQ ID NOS:
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for Windows Version 4.0
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RESULT 5
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; ORGANISM: Human
US-10-027-632-202236
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Best Local :
                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 202237
LENGTH: 702
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LENGTH: 702
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTMARE: FASTSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR ETILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
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                                                                                                                                                                                                                                                                                                                   ORGANISM: Human
                                                                                                                                                                                                                                             Local
                                                                           607 AAAAAAAAATGTTTCCCTAG 588
                                                                                                                                                  667 GGAGTACATTTTAGCATCCTTTTTTTTAGTTCTGTAATAAGGAGATTGTAAATACATTTA
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                                                                                                          71 AAAAAACGGTATTTCCCTGG 90
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Similarity 61.2%;
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Pred. No. 11;
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Pred. No. 11;
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Sequence 6, Application US/09952213D Publication No. US20030096240A1 GENERAL INFORMATION:

APPLICANT: MURAD, FERID APPLICANT: SHARINA, IRAIDA APPLICANT: KRUMENACKER, J. APPLICANT: MARTIN, E.

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PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
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Best Local
                                                                                                                                                                                                                                                                                                                       SEQ ID NO 245609
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CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR FILING DATE: 2000-07-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
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CURRENT APPLICATION UNMBER: US/09/952,213D
CURRENT FILING DATE: 2002-08-16
NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                                                         SOFTWARE: FastSEQ
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1999-08-09
                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
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NAME/KEY: modified_base
LOCATION: (2293..144567)
OTHER INFORMATION: N = A, C,
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TYPE: DNA
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es 53; Conser
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413 TTTTTGGTAGAGATAGGGTTTTGCCATGTTTC
                                       62 ATACAGTTAAAAAAACGGTATTTCCCTGGTTC 93
                                                                                                     2 AAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTA 61
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55; Conserv
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                                                                          Conservative
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Pred. No. 1
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                                                                                                                                                         Mismatches
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; ORGANISM: Human
US-10-027-632-320680
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; ORGANISM: Ovis
US-10-109-551-3
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 Matches
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 320680
LENGTH: 585
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Publication No. US20020194635A1
GENERAL INFORMATION:
                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/193,483 PRIOR FILING DATE: 2000-03-29 PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION NUMBER: 60/280,549
PRIOR FILING DATE: 2001-03-30
NUMBER OF SEQ ID NOS: 10
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CURRENT FILING DATE: 2002-03-28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DUNNE, APPLICANT: PIEDRA
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                                                                                                                  TYPE:
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 Local Similarity
nes 46; Conserv
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nes 45; Conserv
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                                                                                                                                                                                                                        FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
                                                                                                                                                                                                                                                                                  FILING DATE: 2000-02-24
APPLICATION NUMBER: US 60/167,363
FILING DATE: 1999-11-23
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 60/156,358
                                                                                                                  DNA
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62.2%;
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Score 29.2; D
Pred. No. 25;
0; Mismatches
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Pred. No. 81;
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 28;
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US-10-027-632-79603/c
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PRIOR FILLING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILLING DATE: 2000-03-29
PRIOR PPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
                                                                                                                                                                                                                                                                   Sequence 3, Application US/09801876B
Patent No. US20020127683A1
GENERAL INFORMATION:
APPLICANT: YE, Jane et al
                                                                                              SOFTWARE: FastSEQ for SEQ ID NO 3
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SOFTWARE: FRSTSEQ for Windows Version 4.0
SEQ ID NO 79603
LENGTH: 1270
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                                                                                                                                                                                                             TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND TITLE OF INVENTION: THEREOF
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/801,876B CURRENT FILING DATE: 2001-03-09
                                                                                                                                                                                           FILE REFERENCE: CL001160
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE:
                                                           TYPE: DNA
                     FEATURE:
                                       ORGANISM: Human
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NAME/KEY: misc_feature
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46; Conser
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                                                                                                              Windows Version 4.0
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Pred. No. 32;
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Best Local :
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RESULT 12
US-10-027-632-11949/c
                                         CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
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US-10-254-869-3/c
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                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS:
SOFTWARE: FastSEQ for
SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PITITLE OF INVENTION: THEREOF FILE REFERENCE: CL001160DIV
                       PRIOR APPLICATION NUMBER: US 60/185,218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/254,869
CURRENT FILING DATE: 2002-09-26
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LOCATION: (1)...(148567)
OTHER INFORMATION: n = A,T,C or
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FILING DATE:
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2000-02-24
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Pred. No. 1.5e+02
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Pred. No. 1.5e+02;
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RESULT 13
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; ORGANISM: Human
US-10-027-632-11949
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LENGTH: 687
                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
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PRIOR FILING DATE: 1995-04-21
NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/329,960 CURRENT FILING DATE: 2003-01-02 PRIOR APPLICATION NUMBER: US 09/643,990 PRIOR FILING DATE: 2000-08-23 PRIOR APPLICATION NUMBER: US 08/487,429 PRIOR FILING DATE: 1995-06-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Nucleotide Sequence of the Haemophilus influenzae Rd Genome, TITLE OF INVENTION: Thereof, and Uses Thereof
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PRIOR APPLICATION NUMBER: US
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                                                              NAME/KEY: misc_feature
LOCATION: (36543)...(36543)
OTHER INFORMATION: n equals
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LOCATION: (29298)..(29298)
OTHER INFORMATION: n equals
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LOCATION: (10150)..(10150)
OTHER INFORMATION: n equals
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LOCATION: (4747)...(4747)
OTHER INFORMATION: n equals
NAME/KEY: misc_feature
LOCATION: (36551)..(36551)
OTHER INFORMATION: n equals
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LOCATION: (9921)...(9921)
OTHER_INFORMATION: n equals
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LOCATION: (65313)..(65313)
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LOCATION: (80024)..(80024)
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LOCATION: (65309)..(65309)
OTHER INFORMATION: n equal
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LOCATION: (55369)..(55369)
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LOCATION: (51786)..(51786)
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LOCATION: (51602). (51602)
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NAME/KEY: misc_feature
LOCATION: (147197)...(147197)
OTHER INFORMATION: n equals
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LOCATION: (145942)..(145942)
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LOCATION: (145171)..(145171)
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LOCATION: (145058)..(145058)
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LOCATION: (142750)..(142750)
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LOCATION: (122336)..(122336)
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LOCATION: (131360)..(131360)
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LOCATION: (131340)...(131340)
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LOCATION: (122167)...(122167)
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LOCATION: (121344)..(121344)
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LOCATION: (120038)..(120038)
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LOCATION: (119924)..(119924)
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LOCATION: (119750)..(119750)
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LOCATION: (117136)..(117136)
OTHER INFORMATION: n equals
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LOCATION: (107248)..(107248)
OTHER_INFORMATION: n equals a,
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LOCATION: (105121)..(105121)
OTHER INFORMATION: n equals a
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COCATION: (140398)..(140398)
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OCATION: (139910)..(139910)
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RESULT 14
US-10-114-170-215/c
; Sequence 215, Appl.;
; Publication NS
SEQUENCE DESCRIPTION: SEQ ID NO: 215: US-10-114-170-215
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Best Local
                                                                                                                         INFORMATION FOR SEQ ID NO: 215
SEQUENCE CHARACTERISTICS:
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LOCATION: (152500)..(152500)
OTHER INFORMATION: n equals
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LOCATION: (152530)..(152530)
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                                                                                                                                                                                                                         APPLICATION NUMBER: 09/453,702
FILING DATE: 03-DEC-1999
APPLICATION NUMBER: 60/110,955
FILING DATE: 04-DEC-198
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J
REGISTRATION NUMBER: 27386
                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 251-5000
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/10/114,170
FILING DATE: 01-Apr-2002
CLASSIFICATION: -Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Word Perfect 8.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NO. US20030023075Aiel Sequences of E. coli 0157 NUMBER OF SEQUENCES: 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 AAAACGGTATTTCCCTGGTTCTGATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13 ATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAA 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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                                                                        STRANDEDNESS: double
                                                                                       TYPE: nucleic acid
                                                                                                                                                          TELEFAX: (608)
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Diskette, 3.50 inch. COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                        TOPOLOGY:
                                                                                                       LENGTH: 2692
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Plunkett, bu,
Ah, Rod
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58.0%;
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RESULT 15
US-09-989-722-106/c
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                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-04-28
PRIOR FILING DATE: 1998-04-28
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CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/06250
PRIOR APPLICATION NUMBER: 60/065186
PRIOR PILING DATE: 1997-10-17
PRIOR PILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
PRIOR FILING DATE: 1997-11-12
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                                        OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR FILING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
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      FILING DATE:
APPLICATION N
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Kljavin, Ivar J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhang, Zemin
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Stewart, Timothy A.
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      60/087759
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Pred. No. 72;
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/
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PRIOR APPLICATION NUMBER: 60/089514
OR APPLICATION NUMBER: 60/089653
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089801
OR APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/088212
FILING DATE: 1998-06-05
APPLICATION NUMBER: 60/088217
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APPLICATION NUMBER: 60/088326
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: .60/
FILING DATE: 1998-06-17
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FILING DATE: 1998-06-11
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FILING DATE: 1998-06-10
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FILING DATE:
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APPLICATION NUMBER: 60/090863
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APPLICATION NUMBER: 60/091360
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/091626
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
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   46;
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 Score 28; DB Pred. No. 53; 0; Mismatches
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RESULT 16
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/065186
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OR FILING DATE: 1997-11-13
OR APPLICATION NUMBER: 60/066770
OR FILING DATE: 1997-11-24
OR APPLICATION NUMBER: 60/075945
OR FILING DATE: 1998-02-25
OR APPLICATION NUMBER: 60/078910
OR APPLICATION NUMBER: 60/078910
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R APPLICATION NUMBER:
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Godowski, Paul
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Stewart, Timothy A.
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; Patent No. US20020072496A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
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APPLICATION NUMBER: 60/075945
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Baker, Kevin P.
Botstein, David
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Godowski, Paul J.
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art, Timothy A.
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OR APPLICATION NUMBER: 60/089105
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OR APPLICATION NUMBER: 60/089440
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/089801
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FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/088742
FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/0
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FILING DATE: 1998-06-05
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Query Match
Best Local
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090444
FILING DATE: 1998-06-24
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090431
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
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FILING DATE: 1998-06-26
APPLICATION NUMBER: 60/091360
FILING DATE: 1998-07-01
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APPLICATION NUMBER: 60/090690
FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090676
FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090472
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FILING DATE: 1998-07-07
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FILING DATE: 1998-06-23
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Pred. No. 53;
                                                                                                            Mismatches
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CURRENT FILING DATE: 2001-11-19
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PR FILING DATE: 1998-06-02
PR FILING DATE: 1998-06-02
PR APPLICATION NUMBER: 60/087759
PR APPLICATION NUMBER: 60/087827
PR APPLICATION UNMBER: 60/087827
PR FILING DATE: 1998-06-03
PR FILING DATE: 1998-06-03
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APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
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FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/0
FILING DATE: 1998-02-25
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                               APPLICATION NUMBER: FILING DATE: 1998-00 APPLICATION NUMBER:
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FILING DATE: 1998-03-20
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Godowski, Paul J
Grimaldi, J.Christopher
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Gerber, Hanspeter
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Stewart, Timothy
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RAPPLICATION NUMBER: 60/089532

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PR APPLICATION NUMBER: 60/088029

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PR FILING DATE: 1998-06-04

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DR APPLICATION NUMBER: 60/090694
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Qy В 밁 δÃ Matches Query Match Best Local : 156 216 65 CAGTTAAAAAAACGGTA 81 46; Similarity CCCTGTAAAAAATAGTA 140 TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA TGAGTGGTTNAAATCTTTCATGGTGGGATAAATAACAGCTGCATCTATGATAATCCACCA Conservative 27.2%; 59.7%; Score 28; DB Pred. No. 53; 0; Mismatches 0; 9 31; Length 466 Indels 0; Gaps

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CURRENT APPLICATION NUMBER: US/09/989,731
CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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PRIOR APPLICATION NUMBER: 60/065311
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US-09-989-731-106/c
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APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C70
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OR FILING DATE: 1998-06-04
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Stewart, Timothy A.
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FILING DATE: 1998-06-11
APPLICATION NUMBER: 60/088861
FILING DATE: 1998-06-11
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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/088734
FILING DATE: 1998-06-10
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FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/091982
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PRIOR APPLICATION NUMBER: 60/065186
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CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILE STEEL 1002-07
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APPLICANT: Baker, Kevin P.
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APPLICATION NUMBER: 60/087607
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APPLICATION NUMBER: 60/084600
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Stewart, Timothy
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PRIOR FILING DATE: 1997-10-17
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TILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TILE OF INVENTION: Acids Encoding the Same
TLE REFERENCE: P2730P1C15
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Baker, Kevin P.
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Godowski, Paul J.
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APPLICATION NUMBER: 60/089105 FILING DATE: 1998-U5-1
APPLICATION NUMBER: 60
APPLICATION 1998-06-1 FILING DATE: APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-06-FILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: 60/1 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-09 APPLICATION NUMBER: FILING DATE: 1998-06-10 FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-06-10 APPLICATION NUMBER: FILING DATE: 1998-06-10 APPLICATION NUMBER: FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/088167 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/088202 NUMBER: 60/090355: 1998-06-23 NUMBER: 60/090429 : 1998-06-24 NUMBER: 60/090254 NUMBER: 60/090252 : 1998-06-17 1998-06-1998-06-22 1998-06-19 NUMBER: 60/089538 1998-06-17 1998-06-1 1998-06-11 1998-06-1998-06-10 60/090246 60/090349 60/088861 60/088858 60/088826 60/088824 60/088742 60/088738 60/088655 60/088217 60/088810 60/088734 60/088212

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RESULT 22
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                                                               Sequence 106, Application US/09990442 Patent No. US20020132252A1
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APPLICANT:
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                                Ashkenazi, Avi J.
Botstein, David
                  Baker, Kevin P
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Stewart, Timothy A.
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Kljavin, Ivar J.
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Eaton, Dan L.
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FILING DATE: 1998-07-02
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156 CCCTGTAAAAAATAGTA 140
                       65 CAGTTAAAAAAAACGGTA 81
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Ashkenazi, Avi J.
Baker, Kevin P.
Botstein, David

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Eaton, Dan L. Desnoyers,Luc Ferrara, Napoleone

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CURRENT APPLICATION NUMBER: US/09/91,163
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PELING DATE: 1997-10-17
PRIOR PPLICATION NUMBER: 60/062250
PRIOR PILING DATE: 1997-10-17
PRIOR PPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR PPLICATION NUMBER: 60/065311
PRIOR PPLICATION NUMBER: 60/066770
PRIOR PPLICATION NUMBER: 60/066770
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and
TITLE OF INVENTION: Acids Encoding the Same
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OR APPLICATION NUMBER: 60/087827
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
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Godowski, Paul J.
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APPLICATION NUMBER: 60/089947
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Baker, Kevin P.
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Gerber, Hanspeter
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APPLICATION NUMBER: 60/088212
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APPLICATION NUMBER: 60/084600
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Godowski, Paul J.
Grimaldi, J. Christopher
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Stewart, Timothy
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DR FILING DATE: 1998-07-02

PR APPLICATION NUMBER: 60/091978

DR FILING DATE: 1998-07-07

DR APPLICATION NUMBER: 60/091982

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Goddard, Audrey
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Ferrara, Napoleone
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PRIOR PRIOR

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FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-18

PRIOR

APPLICATION NUMBER: 60/089600 FILING DATE: 1998-06-17 APPLICATION NUMBER: 60/089653 APPLICATION NUMBER: 60/089599 FILING DATE: 1998-06-17

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APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-17

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FILING DATE: 1998-06-17

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OR APPLICATION NUMBER: 60/089512
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089514
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089532
OR FILING DATE: 1998-06-17

PRIOR PRIOR

APPLICATION NUMBER: 60/089440 FILING DATE: 1998-06-16

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FILING DATE: 1998-0 APPLICATION NUMBER:

1998-06-10

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APPLICATION NUMBER: APPLICATION NUMBER: 60 FILING DATE: 1998-06PRIOR

APPLICATION NUMBER: FILING DATE: 1998-06-10 PRIOR PRIOR PRIOR PRIOR

FILING DATE: 1998-0 APPLICATION NUMBER:

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FILING DATE: 1998-06-09
APPLICATION NUMBER: 60/C
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OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/09
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RR APPLICATION NUMBER: 60/08
RR FILING DATE: 1998-06-19
RR APPLICATION NUMBER: 60/08
RR FILING DATE: 1998-06-22
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APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
APPLICATION NUMBER: 60/089948
FILING DATE: 1998-06-19
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R APPLICATION NUMBER: 60/01
R FILLING DATE: 1998-06-18
RR APPLICATION NUMBER: 60/01
RR FILING DATE: 1998-06-18
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CURRENT FILING DATE: 2001 11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06770
PRIOR FILING DATE: 1997-11-24
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088212
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088217
OR FILING DATE: 1998-06-05
OR APPLICATION NUMBER: 60/088655
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OR FILING DATE: 1998-06-04
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OR FILING DATE: 1998-04-28
OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
OR APPLICATION NUMBER: 60/087607
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FILING DATE: 1998-06-04
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Roy, Margaret Ann
Stewart, Timothy
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Kljavin, Ivar J
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Williams, P. Mickey
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PRIOR OR FILING DATE: 1998-06-22
OR APPLICATION NUMBER: 60/090252
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OR FILING.DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089600
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OR FILING DATE: 1998-06-17
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APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089598
FILING DATE: 1998-06-17 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/089512 FILING DATE: 1998-06-16 APPLICATION NUMBER: 60/090435 FILING DATE: 1998-06-24 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: FILING DATE: 1998-06 APPLICATION NUMBER: APPLICATION NUMBER: 60/090444 FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/090246 FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: FILING DATE: 1998-06 FILING DATE: 1998-06-10 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088824 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088810 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/088858 NUMBER: 60/090535 NUMBER: 60/088738: 1998-06-10 NUMBER: 60/090472 момвек: 60/089599 : 1998-06-17 NUMBER: 60/090540 NUMBER: 60/089532 1998-06-17 1998-06-16 1998-06-11 1998-06-11 1998-06-10 60/090445 60/089514 60/088876 60/089105 60/088826 60/088742

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APPLICANT: Ashkenaz
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/091626 FILING DATE: 1998-07-02 APPLICATION NUMBER: 60/091633
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                           Goddard, Audrey
Godowski, Paul J.
Grimaldi, J.Christopher
                                                                       Gerritsen, Mary E
                                                                                                      Fong, Sherman
                                                                                                                                 Desnoyers, Luc
Eaton, Dan L.
                                                                                                                                                           Baker, Kevin P.
Botstein, David
Gurney, Austin 1
Kljavin, Ivar J
                                                                                       Gerber, Hanspeter
                                                                                                                  Ferrara, Napoleone
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Roy, Margaret Ann
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RESULT 27
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Baker, Kevin P.
                                                          Grimaldi, J.Christopher Gurney, Austin L.
                                                                                   Goddard, Audrey
Godowski, Paul J.
                                                                                                           Gerber, Hanspeter
Gerritsen, Mary E
                                                                                                                                                             Eaton, Dan L.
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Paoni,Nicholas
Roy, Margaret A
                         Pan,James
                                  Napier, Mary A.
                                                Kljavin, Ivar J
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PRIOR APPLICATION NUMBER: 60/049787
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Gurney, Austin L.
Kljavin, Ivar J.
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Goddard, Audrey
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CURRENT FILING DATE: 2001-11-20
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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OR APPLICATION NUMBER: 60/084600
OR FILING DATE: 1998-05-07
OR APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/088021
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Baker, Kevin P.
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                                  Roy,
Stewart, 'i...
Tas, Daniel
Watanabe, Colin K. Williams, P. Mickey Wood, William I.
                                                                                                                                           Gurney, Austin L.
Kljavin, Ivar J.
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                                                                                                                                                                                                                                       Gerber, Hanspeter
                                                           Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                           Napier, Mary A.
                                                                                                                                                                         Grimaldi, J.Christopher
                                                                                                                                                                                            Godowski, Paul J.
                                                                                                                                                                                                                                                         Fong, Sherman
                                                                                                                                                                                                                                                                        Ferrara, Napoleone
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                                                                                             Paoni, Nicholas F.
                                                                                                               Pan, James
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CURRENT APPLICATION NUMBER: US/09/989/735
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/066770
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945 OR APPLICATION NUMBER: 60/087759
OR FILING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087827
OR FILING DATE: 1998-06-03
OR APPLICATION NUMBER: 60/088021
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088025
OR FILING DATE: 1998-06-04
OR APPLICATION NUMBER: 60/088026
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DR FILLING DATE: 1998-03-20
DR APPLICATION NUMBER: 60/083322
DR FILLING DATE: 1998-04-28
DR APPLICATION NUMBER: 60/084600
DR FILLING DATE: 1998-05-07 R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-06-05
R APPLICATION NUMBER: 60/08
R FILING DATE: 1998-06-05 OR APPLICATION NUMBER: 60/087106
OR FILLING DATE: 1998-05-28
OR APPLICATION NUMBER: 60/087607
OR FILLING DATE: 1998-06-02
OR APPLICATION NUMBER: 60/087609
OR APPLICATION NUMBER: 60/087609
OR FILLING DATE: 1998-06-02 R FILING DATE: 1998-06 R APPLICATION NUMBER: (R FILING DATE: 1998-06-R APPLICATION NUMBER: (FILING DATE: 1998-0-10
APPLICATION NUMBER: 60/C
APPLICATION NUMBER: 60/C FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: 60/088029
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088030
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033 REFERENCE: P2730P1C61 APPLICATION NUMBER: FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-09 APPLICATION NUMBER: 60/088734 APPLICATION NUMBER: APPLICATION NUMBER: 60/088217 FILING DATE: 1998-06-05 APPLICATION NUMBER: 60/0 FILING DATE: 1998-06-05 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 INVENTION: Secreted and Transmembrane Polypeptides and Nucleic INVENTION: Acids Encoding the Same 1998-06-10 1998-06-10 1998-06-10 1998-06-04 60/088824 60/088810 60/088212 60/088202 60/088326 60/088826 60/088655 60/088167 60/088742 60/088028 PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DR FILING DATE: 1998-06-23

DR APPLICATION NUMBER: 60/090355

DR FILING DATE: 1998-06-23

DR APPLICATION NUMBER: 60/090429

DR FILING DATE: 1998-06-24

DR APPLICATION NUMBER: 60/090431

DR FILING DATE: 1998-06-24 OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089908
OR FILING DATE: 1998-06-18
OR APPLICATION NUMBER: 60/089947
OR FILING DATE: 1998-06-19
OR APPLICATION NUMBER: 60/089948
OR APPLICATION NUMBER: 60/089948
OR APPLICATION NUMBER: 60/089952 FILING DATE APPLICATION FILING DATE:
APPLICATION N APPLICATION NUMBER: FILING DATE: 1998-01 APPLICATION NUMBER: FILING DATE: APPLICATION NUMBER: FILING DATE: 1998-01 APPLICATION NUMBER: APPLICATION NUMBER: 60/090349 APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254 APPLICATION NUMBER: FILING DATE: FILING DATE: APPLICATION NUMBER: FILING DATE: FILING DATE: APPLICATION NUMBER: APPLICATION FILING DATE: APPLICATION NUMBER: 60/ FILING DATE: 1998-06-24 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-22 FILING DATE: 1998-0: APPLICATION NUMBER: FILING DATE: 1998-0: FILING DATE: 1998-0 APPLICATION NUMBER: FILING DATE: 1998-06-1 APPLICATION NUMBER: 60/089532
FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089538
FILING DATE: 1998-06-17 APPLICATION APPLICATION APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: FILING DATE: FILING DATE: 1998-00 APPLICATION NUMBER: FILING DATE: 1998-06-19 APPLICATION NUMBER: 60/088861 FILING DATE: 1998-06-11 APPLICATION NUMBER: 60/088876 NUMBER: NUMBER: NUMBER: NUMBER: 60/090445 ...лыЕR: 60/089653 : 1998-06-17 NUMBET 1998-06-24 1998-06-25 1998-06-24 1998-06-24 1998-06-24 1998-06-24 1998-06-25 1998-06-24 1998-06-24 1998-06-18 1998-06-1998-06-17 1998-06-1998-06-16 1998-06-12 1998-06--90-866 60/09069 60/090690 60/090678 60/090557 60/090542 60/090540 60/090444 60/090535 60/090435 60/090676 60/090472 60/089600 6-17 60/090246 60/089801 60/089599 6-17 60/089598 60/089514 60/089512 60/089440 60/089105 60/088876

60/065186

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Best Local
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             TITLE OF INVENTION:
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REFERENCE: P2730P1C19
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
FILING DATE: 1998-07-09
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION:
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                                             Zhang, Zemin
                                                                           Watanabe, Colin K. Williams, P. Mickey
                                                                                                            Tumas,
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Roy, Margaret Ann
Stewart, Timothy A.
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Kljavin, Ivar J.
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Grimaldi, J. Christopher
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Botstein, David
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                                                          Wood, William I.
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          Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same
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CURRENT FILING DATE: '2001-11-14
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PRIOR FILING DATE: 1997-11-12
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FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/
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FILING DATE: 1998-06-10
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APPLICATION NUMBER: 60/088738
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FILING DATE: 1998-06-05
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FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088021
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FILING DATE: 1998-06-02
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FILING DATE: 1998-05-28
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APPLICATION NUMBER:
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                                                        APPLICATION NUMBER: 60/
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                                         FILING DATE: 1998-06-11
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60/087827 60/087759 60/087607 60/087106 60/084600 60/083322 60/078910 60/075945

60/088861 60/088858 60/088826 60/088810 60/088742 60/088734 60/088655 60/088217 60/088202 60/088167 60/088326 60/088033 60/088030 60/088029 60/088028 60/088026 60/088025

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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/
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FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
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FILING DATE: 1998-06-19
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FILING DATE: 1998-06-18
APPLICATION NUMBER: 60/089947
FILING DATE: 1998-06-19
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APPLICATION NUMBER: 60/089532
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FILING DATE: 1998-06-17
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RESULT 31
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APPLICANT:
APPLICANT:
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            APPLICANT: Zhang, Zemin TITLE OF INVENTION: Secreted and Transmembrane TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C53
CURRENT APPLICATION NUMBER: US/09/91,181
CURRENT FILING DATE: 2001-11-16
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PRIOR APPLICATION NUMBER: 60/049787
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APPLICATION NUMBER: 60/091519
FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091626
FILING DATE: 1998-07-02
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FILING DATE: 1998-07-09
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FILING DATE: 1998-07-02
APPLICATION NUMBER: 60/091978
FILING DATE: 1998-07-07
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FILING DATE: 1998-06-25
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Kljavin, Ivar J.
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Wood, William I.
                                                                                                                                                  Tumas,
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Stewart, Timothy A.
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o. US20020197615A1
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| PRIOR APPLICATION NUMBER: 00/0900/0 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090678 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090690 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090694 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090695 PRIOR APPLICATION NUMBER: 60/090695 PRIOR FILING DATE: 1998-06-25 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090696 PRIOR FILING DATE: 1998-06-25 PRIOR APPLICATION NUMBER: 60/090862 | APPLICATION NUMBER: FILING DATE: 1998-0) APPLICATION NUMBER: FILING DATE: 1998-0 | PRIOR APPLICATION NUMBER: 60/089947 PRIOR APPLICATION NUMBER: 60/089948 PRIOR FILING DATE: 1998-06-19 PRIOR APPLICATION NUMBER: 60/089948 PRIOR APPLICATION NUMBER: 60/089952 PRIOR APPLICATION NUMBER: 60/089952 PRIOR APPLICATION NUMBER: 60/090246 PRIOR FILING DATE: 1998-06-22 PRIOR FILING DATE: 1998-06-22 PRIOR FILING DATE: 1998-06-22 PRIOR FILING DATE: 1998-06-22 PRIOR APPLICATION NUMBER: 60/090254 PRIOR APPLICATION NUMBER: 60/090349 PRIOR APPLICATION NUMBER: 60/090349 PRIOR APPLICATION NUMBER: 60/090349 PRIOR FILING DATE: 1998-06-23 PRIOR FILING DATE: 1998-06-23 PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090429 PRIOR APPLICATION NUMBER: 60/090429 PRIOR APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/090431 PRIOR FILING DATE: 1998-06-24 PRIOR APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/090431 PRIOR APPLICATION NUMBER: 60/090431 PRIOR FILING DATE: 1998-06-24 | APPLICATION N FILING DATE: APPLICATION N |

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APPLICANT: Ashkenaz
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CURRENT APPLICATION NUMBER: US/09/989,730 CURRENT FILING DATE: 2001-11-20 PRIOR APPLICATION NUMBER: 60/049787 PRIOR FILING DATE: 1997-06-16 PRIOR APPLICATION NUMBER: 60/062250 PRIOR FILING DATE: 1997-10-17
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                                                                                                    APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C69
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APPLICATION NUMBER: 60/
FILING DATE: 1998-07-01
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Baker, Kevin P.
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Williams, P. Mickey
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Roy, Margaret Ann
Stewart, Timothy A.
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APPLICATION NUMBER: 60/091478 FILING DATE: 1998-07-01 APPLICATION NUMBER: 60/091360

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OR APPLICATION NUMBER: 60/090676
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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Williams, P. Mickey
Wood, William I.
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Grimaldi, J.Christopher
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PR APPLICATION NUMBER: 60/083322

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PR APPLICATION NUMBER: 60/087609

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RESULT 34
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               APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT ELING DATE: US/09/993,687
CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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OR APPLICATION NUMBER: 60/091978
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OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
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Godowski, Paul J.
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FILING DATE: 1998-06-17
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FILING DATE: 1998-06-1
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P273091264
CURRENT APPLICATION NUMBER: US/09/989,734
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/06787
PRIOR APPLICATION NUMBER: 60/062250
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065186
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
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APPLICANT: Baker,Kevin P.
APPLICANT: Botstein,David
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DR FILING DATE: 1998-07-02
DR APPLICATION NUMBER: 60/991978
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/091982
DR FILING DATE: 1998-07-07
DR APPLICATION NUMBER: 60/092182
APPLICATION NUMBER: 60/075945 FILING DATE: 1998-02-25
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FILING DATE: 1998-07-02
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FILING DATE: 1998-07-02
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INVENTION: Secreted and Transmembrane
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Roy, Margaret Ann
Stewart, Timothy A.
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Kljavin, Ivar J.
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| NUMBER: 6: : 1998-06- | NUMBER: 6: : 1998-06- | NUMBER: 60/ : 1998-06-17 | : 1998-06-16 | : 1998-06-16 | NUMBER: 60/ | NUMBER: 60/ | : 1998-06-12 | NUMBER: 60/ | NUMBER: 60/ | : 1998-06-11 | NUMBER: 60/ | NUMBER: 60/ | : 1998-06- | | NUMBER: 6 | : 1998-06- | : 1998-06- | N NUMBER: 60/088742 | NUMBER: 6 | : 1998-06- | NIMBER: 6 | NUMBER: 60 | : 1998-06-(| : 1998-06-05 | NUMBER: 60/0 | NUMBER: 60/C | : 1998-06-05 | 1998-06-04 | NUMBER: 60/0 | NUMBER: 60/C | : 1998-06-04 | 1998-06-04 | : 1998-06-04 NUMBER: 60/08 | NUMBER: 60/08 | NUMBER: 60/0 | : 1998-06-04 | : 1998-06-04 | NUMBER: 60/C | NUMBER: 60 | : 1998-06-02 | NUMBER: 60/C | NUMBER: 60/0 | : 1998-06-02 | : 1998-05-28 | NUMBER: 60/C | NUMBER: 60/0 | N NUMBER: 60/08 | : 1998-03-20 |
| 0/089598 17 | 19538 | 089532 | 007514 | 0514 | 089512 | 089440 | | 089105 | 088876 | | 088861 | 85880 |) | 18826 | 8824 | 10 | | 8742 | 8738 | | 8734 | 8655 |)5 | 8317 | 88212 | 88202 | 79188 | 1 | 88326 | 88033 | 8030 | | . 8029 | 8028 | 88026 | i | 88025 | 88021 | 7087827 | | 187759 | 87609 | 0.00 | 7607 | 87106 | 84600 | 83322 | |
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PRIOR

APPLICATION NUMBER: 60/090695 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090696

APPLICATION NUMBER: 60/090690 FILING DATE: 1998-06-25 APPLICATION NUMBER: 60/090694 FILING DATE: 1998-06-25

OR FILING DATE: 1998-06-25
OR APPLICATION NUMBER: 60/090862
OR FILING DATE: 1998-06-26
OR APPLICATION NUMBER: 60/090863
OR APPLICATION NUMBER: 60/091360
OR FILING DATE: 1998-07-01
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OR APPLICATION NUMBER: 60/090429
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60/089948 6-19 60/089952 APPLICATION NUMBER: 60/089801 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/089907 FILING DATE: 1998-06-18

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APPLICATION NUMBER: 60/089599
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APPLICATION NUMBER: 60/089600
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PRIOR APPLICATION NUMBER: 60/04787
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Roy, Margaret Ann
Stewart, Timothy A.
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Godowski, Paul J.
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OR APPLICATION NUMBER: 60/091978
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/091982
OR FILING DATE: 1998-07-07
OR APPLICATION NUMBER: 60/092182
OR FILING DATE: 1998-07-09
                 FILING DATE: 1998-03-20
APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
                                                                                                                APPLICATION NUMBER: 60/066770 FILING DATE: 1997-11-24
APPLICATION NUMBER:
                                                                                                 APPLICATION NUMBER: 60/075945
                                                                 APPLICATION NUMBER: 60/078910
                                                                                 FILING DATE: 1998-02-25
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Williams, P. Mickey
Wood, William I.
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Grimaldi, J. Christopher
                                                                                                                                                                                                                                                                                                                                                                      Zhang, Zemin
                                                                                                                                                                                                                                                                                                                                                                                                                                       Tumas,
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Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gurney,Austin
Kljavin,Ivar J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goddard, Audrey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gerber, Hanspeter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paoni,Nicholas F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pan,James
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Daniel
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; Pred. No. 53;
0; Mismatches
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1998-05-07

60/084600

R FILING DATE: 1998-05-28
R APPLICATION NUMBER: 60/01
R FILING DATE: 1998-06-02
R APPLICATION NUMBER: 60/01
R FILING DATE: 1998-06-02

60/087609 60/087607

E: 1998-05-28 V NUMBER: 60/0

R FILING DATE: 1998-06-03
R APPLICATION NUMBER: 60/0
R FILING DATE: 1998-06-04
R APPLICATION NUMBER: 60/0
R FILING DATE: 1998-06-04

60/088025 60/088021 APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087827

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04

60/088028

APPLICATION NUMBER: 60/088026

PRIOR OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091544
OR FILING DATE: 1998-07-01
OR APPLICATION NUMBER: 60/091519
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091636
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091633
OR FILING DATE: 1998-07-02
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091978
OR APPLICATION NUMBER: 60/091978 OR FILING DATE: 1998-06-23
OR APPLICATION NUMBER: 60/090355
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090429
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090431
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090445
OR FILING DATE: 1998-06-24
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OR FILING DATE: 1998-06-24
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090445
OR APPLICATION NUMBER: 60/090472
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090535
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540
OR FILING DATE: 1998-06-24
OR APPLICATION NUMBER: 60/090540 DR APPLICATION NUMBER: 60/089948
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/08952
DR FILING DATE: 1998-06-19
DR APPLICATION NUMBER: 60/090246
DR FILING DATE: 1998-06-22
DR FILING DATE: 1998-06-22 R FILING DATE: 1998-06-25
R APPLICATION NUMBER: 60/09
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APPLICATION NUMBER: 60/090690 APPLICATION I FILLING DATE: 1998-06-22
APPLICATION NUMBER: 60/090254
FILING DATE: 1998-06-22
APPLICATION NUMBER: 60/090349 FILING DATE: 1998-06-18 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-19 APPLICATION NUMBER: APPLICATION NUMBER: NUMBER: 60/ : 1998-06-26 NUMBER: NUMBER: NUMBER: NUMBER: NUMBER: 60/089801: 1998-06-18 NUMBER: 1998-07-01 1998-06-26 1998-06-24 1998-06-25 1998-06-60/091478 60/090863 969060/09 60/090695 60/090694 60/090557 60/091360 60/090676 60/090678 60/090252 60/089947 806680/09 60/089907

DR APPLICATION NUMBER: 60/088202
DR FILING DATE: 1998-06-05
DR APPLICATION NUMBER: 60/088212
DR FILING DATE: 1998-06-05
DR APPLICATION NUMBER: 60/088217
DR FILING DATE: 1998-06-05

FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1000-06-04 APPLICATION NUMBER: 60/ FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088029 FILING DATE: 1998-06-04

60/088167 60/088326

60/088033 60/088030

FILING DATE: 1998-06-05

FILING DATE: 1998-06-09

APPLICATION NUMBER: 60/0

TITMC DATE: 1998-06-09

60/088655

60/088734

DR FILING DATE: 1998-06-09
PR APPLICATION NUMBER: 60/08
PR FILING DATE: 1998-06-10
PR APPLICATION NUMBER: 60/08
PR FILING DATE: 1998-06-10
PR APPLICATION NUMBER: 60/08
PR APPLICATION NUMBER: 60/08
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APPLICATION NUMBER: 60/1 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/1 FILING DATE: 1998-06-10

60/088824

60/088810 60/088742 60/088738

PRIOR PRIOR PRIOR

FILING DATE: 1998-0 APPLICATION NUMBER:

APPLICATION

NUMBER:

NUMBER: 60/089532 1998-06-17

APPLICATION NUMBER: 60/089514 FILING DATE: 1998-06-16

RIOR FILING DATE: 1998-06-17

IUOR APPLICATION NUMBER: 60/089598

TOR FILING DATE: 1998-06-17

IOR APPLICATION NUMBER: 60/089599

IOR FILING DATE: 1998-06-17

IOR APPLICATION NUMBER: 60/089600

OR APPLICATION NUMBER: 60/089600

OR FILING DATE: 1998-06-17

OR APPLICATION NUMBER: 60/089653

OR FILING DATE: 1998-06-17

OR PPLICATION NUMBER: 60/088826
OR FILING DATE: 1998-06-10
OR APPLICATION NUMBER: 60/08858
OR PILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088861
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/088876
OR FILING DATE: 1998-06-11
OR APPLICATION NUMBER: 60/089105
OR FILING DATE: 1998-06-12
OR APPLICATION NUMBER: 60/089440
OR FILING DATE: 1998-06-16
OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60/089512
OR APPLICATION NUMBER: 60-6-16

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CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-06-250
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-10-17
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/06770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/06770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
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US-09-997-428-106/c
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Best Local S
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2730P1C44
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            FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
FILING DATE: 1998-05-28
                                                                                                APPLICATION NUMBER: 60/078910 FILING DATE: 1998-03-20 APPLICATION NUMBER: 60/083322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46;
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Botstein, David
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe, Colin K. Williams, P. Mickey
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Roy, Margaret Ann
Stewart, Timothy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Napier, Mary A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gurney, Austin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grimaldi, J. Christopher
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ferrara, Napoleone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , Nicholas F.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/
                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/089105
FILING DATE: 1998-06-12
APPLICATION NUMBER: 60/089440
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APPLICATION NUMBER: 60/0
FILING DATE: 1998-06-09
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                                APPLICATION NUMBER: FILING DATE: 1998-0
                                                              APPLICATION NUMBER: 60/
FILING DATE: 1998-06-17
                                                                                                                                  APPLICATION NUMBER: 6 FILING DATE: 1998-06-
                                                                                                                                                                    FILING DATE:
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APPLICATION NUMBER: 60/
FILING DATE: 1998-06-16
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FILING DATE: 1998-06-10
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APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
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Stewart, Timothy A.
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Query Match Best Local Similarity

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Baker, Kevin P.
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Kljavin, Ivar J.
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Williams, P. Mickey
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Roy, Margaret Ann
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Desnoyers, Luc
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APPLICATION NUMBER: 60/090252 FILING DATE: 1998-06-22 APPLICATION NUMBER: 60/090254

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CURRENT FILING DATE: 2001-11-14
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PRIOR FILING DATE: 1997-10-11
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
APPLICATION NUMBER: 60/087609
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APPLICATION NUMBER: 60/088021 FILING DATE: 1998-06-04
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Stewart, Timothy A.
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Query Match 27.2%; Score 28; DB 11; Length 466; Best Local Similarity 59.7%; Pred. No. 53; Matches 46; Conservative 0; Mismatches 31; Indels 0; Gaps

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RESULT 42
US-09-990-711-106/c
; Sequence 106, Application US/09990711
; Publication No. US20030032023A1
. GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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TITLE OF INVENTION: Secreted and Transmembran
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C2
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APPLICATION NUMBER: 60/
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APPLICATION NUMBER: 60/087759
FILING DATE: 1998-06-02
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FILING DATE: 1998-02-25
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 APPLICATION NUMBER: 60/088025 FILING DATE: 1998-06-04
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Stewart, Timothy A.
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IOR APPLICATION NUMBER: 60/089653
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OR APPLICATION NUMBER: 60/089907
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APPLICATION NUMBER: 60/088826
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APPLICATION NUMBER: 60/089598
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FILING DATE: 1998-07-01
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FILING DATE: 1998-06-25
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RESULT 43
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CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
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FILING DATE: 1998-06-04
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
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APPLICATION NUMBER: 60/078910
FILING DATE: 1998-03-20
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FILING DATE: 1997-11-13
APPLICATION NUMBER: 60/066770
FILING DATE: 1997-11-24
APPLICATION NUMBER: 60/075945
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FILING DATE: 1997-10-17
APPLICATION NUMBER: 60/065186
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Kljavin, Ivar J.
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Roy, Margaret Ann
Stewart, Timothy A.
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FILING DATE: APPLICATION :

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OR APPLICATION NUMBER: 60/089907
OR FILING DATE: 1998-06-18
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OR APPLICATION NUMBER: 60/089538
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OR APPLICATION NUMBER: 60/089512
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APPLICATION NUMBER: 60/088734
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APPLICATION NUMBER: 60/088738
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APPLICATION NUMBER: 60/088033
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APPLICATION NUMBER: 60/088326
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APPLICATION NUMBER: 60/091982
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APPLICATION NUMBER: 60/091978
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FILING DATE: 1998-06-25
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FILING DATE: 1998-06-24
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FILING DATE: 1998-06-23
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR PILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Baker, Kevin P.
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APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C28
FILE REFERENCE: P2730P1C28
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FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/084600
FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/087106
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APPLICATION NUMBER: 60/087609
FILING DATE: 1998-06-02
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Godowski, Paul J.
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Gerritsen, Mary E.
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                                                                 60/088029
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OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089538
OR FILING DATE: 1998-06-17
OR APPLICATION NUMBER: 60/089598
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APPLICATION UNMBER: 60/089512
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APPLICATION NUMBER: 60/089440 APPLICATION NUMBER: 60/089908 APPLICATION NUMBER: APPLICATION NUMBER: 60/088810 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088742 APPLICATION NUMBER: 60/088734 FILING DATE: 1998-06-10 APPLICATION NUMBER: 60/088738 FILING DATE: 1998-06-18 FILING DATE: APPLICATION NUMBER: 60/088655 FILING DATE: 1998-06-09 FILING DATE: 1998-06-05 APPLICATION NUMBER: APPLICATION NUMBER: 60/088212 FILING DATE: 1998-06-05 FILING DATE: 1998-06-05 APPLICATION NUMBER: APPLICATION NUMBER: 60/ FILING DATE: 1998-06-05 FILING DATE: 1998-06-04 APPLICATION NUMBER: 60/088033 FILING DATE: 1998-06-04 APPLICATION NUMBER: NUMBER: 1998-06-19 1998-06-19 1998-06-11 1998-06-10 60/089952 60/089948 60/089947 60/088876 60/088217 60/088202 60/088167 60/088326

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RESULT 45
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; Publication No. US20030045463A1
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FILING DATE: 1998-06-25
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APPLICATION NUMBER: 60/090696
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FILING DATE: 198-06-24
APPLICATION NUMBER: 60/090557
FILING DATE: 1998-06-24
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APPLICATION NUMBER: 60/091633
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FILING DATE: 1998-07-01
APPLICATION NUMBER: 60/091519
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                                                                                                                            156
                                                                                                                                                                                                          216 TGAGTGGTTNAAATCTTTCATGGTGGGATAAATAACAGCTGCATCTATGATAATCCACCA 157
                                                                                                                                               65 CAGTTAAAAAAACGGTA 81
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                                                                                                                                                                                                                                                                                             l Similarity
46; Conserv
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PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR PELICATION NUMBER: 60/065186
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DR APPLICATION NUMBER: 60/075945

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DR APPLICATION NUMBER: 60/083322
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APPLICATION NUMBER: 60/088025
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/087607
FILING DATE: 1998-06-02
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APPLICATION NUMBER: 60/087827
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                 FILING DATE: 1998-06-04
APPLICATION NUMBER: 60/088033
FILING DATE: 1998-06-04
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APPLICATION NUMBER: 60/088021
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Botstein, David
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Grimaldi, J. Christopher
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Stewart, Timothy
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DR APPLICATION NUMBER: 60/088167

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APPLICATION NUMBER: 60/089907
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FILING DATE: 1998-06-18
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APPLICATION NUMBER: 60/089532
TTTMC DATE: 1998-06-17
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FILING DATE: 1998-06-23
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-22
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FILING DATE: 1998-06-17
APPLICATION NUMBER: 60/089600
FILING DATE: 1998-06-17
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APPLICATION NOTICE:
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FILING DATE: 1998-06-10
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DR FILING DATE: 1998-06-25

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APPLICATION NUMBER: 60/090862
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APPLICATION NUMBER: 60/090535
FILING DATE: 1998-06-24
APPLICATION NUMBER: 60/090540
                                          APPLICATION NUMBER: 60/091982
FILING DATE: 1998-07-07
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APPLICATION NUMBER: 60/091519
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FILING DATE: 1998-06-26
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NUMBER: 60/092182
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                                                                                    46;
                                                                                    Similarity 59.7
16; Conservative
CCCTGTAAAAAATAGTA 140
                   CAGTTAAAAAAACGGTA 81
                                                   TGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATA 64
                                                                                              27.2%;
59.7%;
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                                                                                  Score 28; DB Pred. No. 53; 0; Mismatches
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Search completed: August 25, Job time : 131 secs 2003, 07:52:45

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Copyright (c) 1993 - 2003 Compugen Ltd.
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ALIGNMENTS

LOCUS

AA897178

ann09e08.sl Soares_NFL_T_GBC_Sl Homo sapiens cDNA clone

IMAGE:1466342 3', mRNA sequence.

ACCESSION

AA897178

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Eukaryocta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tinsert Length: 847

High quality sequence stop: 132.

Jorganism-"Homo sapiens

Location/Qualifiers

ARB97178

238

MRNA linear EST 04-JAN-1999

MRNA linear EST 04-JAN-1999

RETHER CONTENT CO

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REFERENCE
AUTHORS
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AL710553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 713)
Ansorge,W., Wirkner,U., Mewes,W., Weil,B. and Wiemann,S.
EST (Ansorge,W., Wirkner,U., Mewes,H.W., Weil,B. and Wiemann,S.)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL710553
AL710553.1 GI:19693908
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DKFZp686L236_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone DKFZp686L236 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69; Conserv
                                                                                                                                                                                                                                                                Berlin-Charlottenburg, GERMAN
Location/Qualifiers
                                                                                                                                                                                                                                                                                                            No sl sequence available.
This clone (DKFZp686L236) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubherweg 6, 14059
                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone from S. Wiemann, Molecular Genome Analysis, German Can
Research Center (DKFZ); Email s.wiemann@dkfz- heidelberg.de;
sequenced by EMBL (European Molecular Biology Laboratories,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany This is the 5' sequence of the clone insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GAAGTGACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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/clone_lib="Soares_NFL_T_GBC_S1"
/note="Organ: pooled; Vector: p7773D-Pac (Pharmacia) with
/note="Organ: pooled; Vector: p7773D-Pac (Pharmacia) with
a modified polylinker; Site_1: not 1; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NbHL19W, testis NHT, and B-cell
NCI_GGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification reaction. The driver
vitro. Following HAP purification reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
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ص
                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp666L236"
/cissue_type="human skeletal muscle"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Soares and M. Fatima Bonaldo.
1 53 c 45 g 69 t
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
                                                      'lab_host="DH10B"
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Pred. No. 3.6e-05;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                            GERMANY; Email: clone@rzpd.de
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COMMENT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UI-H-DIO-ato-m-19-0-UI.s1 NCI_CGAP_DIO Homo IMAGE:5862330 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
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                                                                                                                                  /clone_lib="NCI_CGAP_DIO"
/clone_lib="NCI_CGAP_DIO"
/clone_"Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; MCI_CGAP_DIO is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the
                      TAG_TISSUE=lung with fibrosis TAG_SEQ=ATACGCGGTC"
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140 c 129
                                                                  TAG_LIB=UI-H-DIO
                                                                                                                 (dT)18 tail. The
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/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                              /lab_host="DH10B (Life Technologies)"
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Pred. No. 4.3e-05;
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Plate: LLAM12323 row: h column:
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Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="IMAGE:5574588"
/clone="IMAGE:5574588"
/tissue_type="duodenal adenocarcinoma, cell line"
/lab_bost="PH108 (phage-resistant)"
/clone_lib="NIH_MGC_88"
/clone_lib="NIH_MGC_88"
/note="Organ: small intestine; Vector: pcMV-SPORT6;
Site_1: NotI; Site_2: SalI; Cloned unidirectionally;
oligo-dT primed. Average insert size 1.767 kb. Library
enriched for full-length clones and constructed by Life
Technologies. Note: this is a NIH_MGC Library."
93 a 209 C 191 g 317 t
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Pred. No. 4.6e-05;
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Homo sapiens cDNA clone IMAGE:5574588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAAGTGACTGGAATAACAGTTTAATGACAGCAFTAATAGCTCCTGCATATGTGAATTGCT
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                                                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                 1123 bp
AGENCOURT_10164573 NIH_MGC_71 Hc
5', mRNA sequence
                   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                        Contact: Robert Strausberg, Ph.D
                                                                                         NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
                                                                                                                                                                                                                              EST
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Tissue Procurement: ATCC
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National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates;
1 (bases 1 to 1083)
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                                                                                                                                                                                                                                             BU517082.1 GI:22824608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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cDNA Library Preparation: Life Technologies,
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                                                                                                                                (bases 1 to 1123)
                                                                                                                                                                                                                                                                               mRNA sequence.
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/mol_type="mRNA"
/mb_xref="taxon:9606"
/clone="IMAGE:5555441"
/tissue_type="leiomyosarcoma"
/tissue_type="leiomyosarcoma"
/lab_host="DHIOB (phage-resistant)"
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/clone_rogan: uterus; Vector: pCMV-SPORT6; Site_1:
/note="Organ: uterus; Vector: bCMV-SPORT6; Site_1:
Site_2: Sali; Cloned unidirectionally. Primer: Ol.
Average insert size 2.1 kb.
34 a 219 c 212 g 318 t
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75.0%;
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Pred. No. 4.7e-05;
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Catarrhini; Hominidae;
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                                                                                           Gene Collection (MGC)
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imer: Oligo dT.
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
Contact: Robert Strausberg,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 491)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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EST.
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AGENCOURT_10612800 NIH_MGC_126 H
IMAGE:6727961 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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http://image.llnl.gov
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
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      /tissue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NH_MCC_126"
/note="Typettor: pDNR-LIB: Site_1: SfiI (ggccattatggcc);
Site_2: SfiI (ggccgcctggcc); Double-stranded cDNA was prepared from a pool of 40 cell line polyA+ RNAs (bladder - 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon
                                                                                                                                                        /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6727961"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 2.1 kb. "
336 c 194 g 310 t
                                                                                                                                                                                                                   /organism="Homo_sapiens"
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_71"
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/mol_type="mRNA"
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: cgapbs-r@mail.nih.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                     /clone_lib="NCI_CGAP_Gas4"
/note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sasite_2: Not1; Cloned unidirectionally. Primer: Oligo
                                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:2140904"
/tissue_type="poorly differentiated
signet ring cell features"
                                        Average insert size 1.69 kb. Life Technologies catalog
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a 75 c
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5'-AAGCAGTGGTATCAACGCAGAGTGGCCATTACGGCCGGG-3' and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kb size fraction (other fractions present in NIH_MGC_127 and NIH_MGC_128). Library created in the laboratory of usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC relation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)NN-3'. Full-length enriched library was constructed using the Clontech Creator SMART kit and size-selected to contain the 0.5-1
                                                                                                                             /lab_host="DH10B"
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RESULT 10
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                                                         174 AAAAAAGGTCTTTCAGTACTTCTCATCTA 146
                                                                                                               433 AATCAATTAAAAAAAAGGTCTTTCAGTACTTCTCATCTA 472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries Osteoarthr. Cartil. 9 (7), 641-653 (2001) 21482651
                                                                                                                                                                            . Similarity
56; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GlaxoSmithKline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Sanjay Kumar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kumar, S., Connor, J.R., Dodds, R.A., Halsey, W., Van Horn, M., Mao, J., Sathe, G., Mul, P., Agarwal, P., Badger, A.M., Lee, J.C., Gowen, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                   Email: sanjay_kumar-l@gsk.com
Seq primer: T7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UW2109
                                                                                     AAAAACGGTATTTCCCTGGTTCTGATCCA 100
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1 56 c
                                                                                                                                                                                                                                                                          /tissue_type="cartilage"
/tab_host="E.coli DHI0 B"
/clone_lib="HOA (Human Osteoarthritic Cartilage)"
/clone_lib="HOA (Human Osteoarthritic Sall; Site_2: No.
/note="Vector: pSPORT I; Site_1: Sall; Site_2: No.
                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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1...256
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Pred. No. 3.1;
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RESULT 11
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IMAGE:2367449
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                                                                                                AI742206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 469.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished Contact: Robert Strausberg, Ph.D.
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                    AI742206.1
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DNA Sequencing by: Washington University Genome
Clone distribution: NCI-CGAP clone distribution
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bonaldo, Ph.D.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 507)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tissue Procurement: Christopher A. Moskaluk, M.D., R. Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library Preparation: M. Bento Soares, Ph.D.,
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                                                                                                                                                                                                AAAAAAGGTCTTTCAGTACTTCTCATCTA 469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                174
                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_GC4 was prepared, and scircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified CDNAs from a pool of 5,000 clones made from the same library (cloneIDS 15,000 clones made from the same library (cloneIDS 1257096-1258631, 1469064-1470983, and 1475592-1476743). Subtraction by Bento Soares and M. Fatima Bonaldo. 88 c 85 g 159 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="pooled germ
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="NCI_CGAP_GC6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:2310168"
                                                Soares_NSF_F8_9W_OT_PA_P_S1 Homo
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62.9%;
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Pred. No. 7.
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                                                                                                                                                                                                                                                                                                                                                            33;
                                                                                                                                                                                                                                                                                                                                                                                                Length 507;
                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                             sapiens cDNA clone
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                                                                                             EST 19-DEC-1999
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Homo sapiens (human)

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REFERENCE
AUTHORS
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Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                        Unpublished
                                                                             NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 607)
                                                                                                                                                                                                                                                                                                                                                                                                                  CA437823 607 bp mRNA linear UI-H-DHO-aur-o-23-0-UI.sl NCI_CGAP_DHO Homo sapiens UI-H-DHO-aur-o-23-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                          EST
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Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 789 Std Error: 0.00
                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                CA437823.1 GI:24802243
                                                                                                                                                                                                                                                                                                                                                                                                     CA437823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 534)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAAAAAGGTCTTTCAGTACTTCTCATCTA 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone-lib="Soares_NSF_F8_9W_OT_PA__S1"
//Clone-lib="Soares_NSF_F8_9W_OT_PA__S1"
//Clone-lib="Soares_NSF_F8_9W_OT_PA__S1"
//Clone-lib="Soares_NSF_F8_9W_OT_PA__S1"
//Clone-lib="Soares_NSF_F8_9W_OT_PA__S1"
//Clone-lib="Soares pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Ecc RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and ss circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and cloneIDs: Soares NbHFP pool 1:
1150407, 151176-152327
14503-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327
150407, 151176-152327
150407, 151176-152327
150407, 151176-152327
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/clone="IMAGE:2367449"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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Pred. No. 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    cDNA clone
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                                                                                                                                                                     REFERENCE
AUTHORS
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BQ772275
LOCUS
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                                                     COMMENT
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BASE COUNT
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 AAAAAAGGTCTTTCAGTACTTCTCATCTA 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              72 AAAAACGGTATTTCCCTGGTTCTGATCCA 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12 AATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAA 71
                                                                                                                                                                                                                                                                                                                                                                 632 bp mRNA linear UI-H-EZ1-bbl-k-24-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens UI-H-EZ1-bbl-k-24-0-UI 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56;
Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                         Unpublished
                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap
National Cancer Institute, Cancer Genome Ana
                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 632)
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                        Tumor
                                                                                                                                                                                                                                                                                                                                        BQ772275.1 GI:21980751
                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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The following repetitive elements were found in this cDNA
sequence: 1-36, >AT_rich#Low_complexity (matched compliment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tissue Procurement: Dr. Jose Mercuende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210
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                                                                                     Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCI_CGAP_DHO is a cDNA library containing the following tissue(s): VS-8 Cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo. Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT/73-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TAG_SEQ=AGATCATTGC"
94 c 99 g
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TAG_LIB-UI-H-DHO
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modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_DH0 is a cDNA library containing the following
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="UI-H-DH0-aur-o-23-0-UI"
/tissue_type="Metastatic Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="NCI_CGAP_DH0"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
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62.9%;
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Pred. No. 7.8;
0; Mismatches
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                                                                                                            Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 607;
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Steven Gitelis/ Rush Presbiterian,

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RESULT 14
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                                                                                                                                                              AL180045.1 GI:7818102
AL180045.1 GI:7818102
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                 Tetraodon
233B02 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity
56; Conser
            Saurin, W. and Weissenbach, J. Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence
                                                                                                                   Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
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Seg primer: M13 FORWARD
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/clone_lib="NCI_CGAP_Ch2"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoR I; Site_2: Not I;
NCI_CGAP_Ch2 is a normalized CDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded CDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT7T3-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
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                                                                                         Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
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62.9%;
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AV404852
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saurin,W., Bernot,A. and Weissenbach,J. Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis Genome Res. 10 (7), 939-949 (2000) 20359837
                     Project='Silkworm Genome Program in MAFF, and Research for the Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for whole ESTdb.
                                                                                                                                                             Genome Research Group
National Institute of Agrobiological Sciences
Anagawa 49-1, Inage, Chiba 263-8555, Japan
Email: kmita@nias.affrc.go.jp
method:uni-directional, sequence direction:se
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                                                                                                                                                                                                                                                                                                                                                Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                             Unpublished
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Bombycoidea; Bombycidae;
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/db_xref="taxon:99883"
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Pred. No. 20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 GGACGTTTTGTCTGTGGTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Seq primer: m13 -40 forward
High quality sequence stop: 402.
Location/Qualifiers
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1 (bas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1 Tel: 314 286 1800 Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stops: 402 Source: IMAGE Consortium, LLNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       464 bp mRNA linear EST 16 yy51h10.s1 Soares_multiple_sclerosis_2NbHMSP Homo sapiens clone IMAGE:277123 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N34305.1 GI:1155447
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAACGGTATTTCCCTGGTTCTG 95
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/clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/note="Vector: pT7T3D (Pharmacia) with a modified
polylinker V_TYPE: phagemid; Site_1: Not I; Site_2: E
; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                  /tissue_type="multiple sclerosis lesions'
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                         /clone="IMAGE:277123"
                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GDB:3895499"
                                                                                                                                                                                                                                                                       /sex="male"
                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Bombyx mori prothoracic gland p50 5th-instar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="female/male mixed"
/tissue_type="prothoracic gland"
/dev_stage="5th-instar day-4 larva"
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/db_xref="taxon:7091"
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/mol_type="mRNA"
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34 TTAAATTAACAAAAACTCAAATTATCTAGTTTT
                        62 ATACAGTTAAAAAAACGGTATTTCCCTGGTTCT 94
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                                                                                                                                                                                                                                                                                                Anagawa 4-9-1, Inage, Chiba 263-8555, Email: kmita@nias.affrc.go.jp
PROJECT = 'CREST project by JST'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56;
                                                                                                                                                                                                                                                                                                                                           Genome Research Group
National Institute of Agrobiological
                                                                                                                                                                                                                                                                                                                                                                       Unpublished
Contact: Mita K
                                                                                                                                                                                                                                                                                                                                                                                                  Mita,K., Morimyo,M., Shimada,T., Okano,K. Establishment of cDNA database of Bombyx 1
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bombyx mori
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bombyx mori (domestic silkworm)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence
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                                                                                                                                                                                                    /strain="p50(Daizo)"
/db_xref="taxon:7091"
/clone="ws00724"
                                                                                                                                                                                                                                            /organism="Bombyx mori"
/mol_type="mRNA"
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G. Becker (NINDS/NIH). "
79 c 77 g 144 t
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139 c 151 g 238 t
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                                                                                                                     31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.8%;
60.2%;
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Pred. No. 34;
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                                                                                                                                                                                                                                                                                                                                                                                                   of Bombyx mori
                                                                                                                                  DB 9;
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57; Conser
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 760)

Delehaunty,K., Fewell,G., Fulton,L., McCombie,W.R., Miner,T., Nash,W., Rabinowicz,P.D. and Wilson,R.K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished. This sequence was generated from the SP6 end of BAC 286A22. 286A22 is part of the Daniokey BAC Library created by R. Plasterk and N.V.
                                  Washington University School of Medicine Email: submissions@watson.wustl.edu Plate: odf92 row: a column: 01 Seq primer: -28RPpOT reverse Class: shotgun
                                                                                                                                                                                                                                                                                                                                                                                                                                              odf92a01.g1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Humphray, S.J., Huckle, E. and Durham, J.L. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Actinopterygii; Neopterygii; Teleostei; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                  Genome Sequencing Center
                                                                                                                                                        Contact: Richard K. Wilson
                                                                                                                                                                                            Whole genome shotgun reads from Brassica oleracea
                                                                                                                                                                                                                                                                                                                                Brassica oleracea
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quality sequence start: 104 quality sequence stop: 279.
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/tissue_type="Testis"
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/db_xref="taxon:7955"
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Whitelaw, C.A., Quackenbush, J.,
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Fax: 301-838-0208
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/note="Vector: pOTw13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thosmas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."
                                                                  /Clone="ZMMBTa391008"
/Clone_lib="ZM_0.6_1.0_KB"
/Clone_Tyector: pCR4-TOPO; Site_1:
/note="vector: pCR4-TOPO; Site_1:
COT selected genomic DNA library"
175 c 157 g 260 t
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/strain="B73"
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: szhao@tijgr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
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Department of Eukaryotic Genomics
The Institute for Genomic Research
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CH230-458D15.TJ CHORI-230 Segment 2
CH230-458D15, genomic survey sequence
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,A., Gebregeorgis,E.,
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GSS.
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                                                                                                                                                                                                   /cell_type="Brain"
/clone_lib="CHOR1-230 Segment 2"
/clone_lib="CHOR1-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: wboI; Site_2:
CHOR1-230 Rat (BN/SSNHSd/MCW) BAC library produce
Pieter de Jong"
a 216 c 163 g 366 t
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/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                            /sex="Female"
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403 AGAGACGCCTTTC
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Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Unr., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter
                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (Dases 1 to 406)
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fp51a12.x3 zebrafish gridded
IMAGE:4759990 3', mRNA sequer
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Creation of genome-wide protein expression libraries using random activation of gene expression
activation of gene expression
activation of gene expression
activation of gene expression
                                                                                                                                                                                                                                         Danio rerio (zebrafish)
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Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
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quality sequence stop
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/clone_see 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression',
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished
Other_ESTs: ft43g05.y1
Other_ESTs. teachen L. Johnson
                                                                                                                                                                                                                  Clark, M., Johnson, S.L., Lehrach, H., Lee, R., Li, F., Marra, M., Eddy, S., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Swaller, M., Swaller, M.,
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                                                                                                                                                                                       Kohn, S., Shin, T., Jackson, Y.,
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Danio rerio
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Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WashU Zebrafish EST
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/note="organ: kidney; Vector: pBK-CMV; Site_1: EcoRI;
Site_2: XhoI; Oligo dT cDNA library constructed from mRNA
pooled from pooled kidney tissue from 300 adult
zebrafish."
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/mol_type="mRNA"
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/lab_host="XLOLR"
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                                                                                                          Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., Eddy,S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwo,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E.,
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IMAGE:5306682 3', mRNA sequenc
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The library was constructed by Dr. Z. Gong. DNA Sequencing by:
Washington University Genome Sequencing Center St. Louis. Please
contact Zhiyuan Gong for further information on this library
(National University of Singapore, Department of Biological
Sciences, Lower Kent Ridge Road, Singapore 119260).
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Contact: Stephen
                     Unpublished
                                           WashU Zebrafish EST Project 1998
                                                                                    Kohn,S., Shin,T., Jackson,Y.; Cardenas,M., McCann,R., Waterston,R
                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases 1 to 570)
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Please contact Zhiyuan Gong for further information on
this library (National University of Singapore,
Department of Biological Sciences, Lower Kent Ridge Road,
Singapore 119260)."

a 106 c 85 g 146 t
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/clone_lib="Gong_zebrafish ovary"
/clone_lib="Gong_zebrafish ovary"
/clone_lib="Gong_zebrafish ovary"
/note="Organ: ovary (pooled); Vector: pBluescript SK-;
Site_1: XhoL; Site_2: EcoRI; Poly A+ RNA was isolatd from
the ovaries of 2 female adult zebrafish (4-5 month old).
cDNAs were made using oligo-dT primers and inserted into
Lambda ZAP II vector (Stratagene) by Dr. Z. Gong, in vivo
mass_excised to pBluescript SK- following the Washington
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/mol_type="mRNA"
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/sex="female"
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                                                                                                                                                                        Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Unpublished
This sequence was generated from the SP6 end of BAC 203G4. 203G4 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details: http://www.sanger.ac.uk/Projects/D_rerio/.
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
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cDNA Library constructed by Library constructed by Invitrogen
donated by R. Campbell (Marine Biology Laboratory, Woods Hole,
DNA Sequencing by: Washington University Genome Sequencing Cen
Clone distribution: the I.M.A.G.E. Consortium/LLNL, send email
                                                                                                                                                                                                                                                                                                                                       Direct Submission
                                                                                                                                                                                                                                                                                                                                                        Humphray, S.J., Huckle, E. and Durham, J.L.
                                                                                                                                                                                                                                                                                                                                                                          Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Danio rerio (zebrafish)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BX192055.1
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Location/Qualifiers
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Fax: 314 286 1810
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: ovary(pooled); Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Whole ovaries collected from zebrafish aged 4-5 months, 1 year and 2 years. Oligo-dT primed, directionally cloned. Average insert size 2 kb. Library constructed by Invitrogen and donated by R. Campbell (Marine Biology Laboratory, Woods Hole, MA)."
                                         /mol_type="genomic DNA"
/db_xref="taxon:7955"
/clone="DKEY-203G4"
                                                                                                                                                      Location/Qualifiers
/note="vector pIndigoBAC-536"
                         /tissue_type="Testis"
                                                                                                            /organism≖"Danio rerio'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="4-5 months, 1 year and 2 years"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Campbel1 zebrafish ovary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:5306682"
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html plate: 414 row: G column: 20
Seg primer: T7
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones availability, please contact Pieter de Jong
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (inf@gresgen.com). BAC end page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K.,
and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: RPCI-23-414G20.TJ
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Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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301 838 0208
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                                                                               /lab_host="hH10B"
/Clone_lib="RPCI-23"
/Clone_lib="RPCI-23"
/Clone_lib="RPCI-23"
/Clone_lib="RPCI-23"
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/Clone_lib="RPCI-23"
/Clone_lib="RPCI-23"
/Clone_lib="RPCI-23"
/Clone_lib="RPCI-23"
/Cloney/Brain; Vector: pBACe3.6; Site_librain genomic DNA was isolated and partially digested brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI wethylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
a 21 c 35 g 66 t
                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:10090"
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30.8; DB 28;
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Salmo salar (Atlantic salmon)
Salmo salar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA preparation and sequencing: Roberto Alberto, Marianne Beetz-Sargent, Maura Busby, Peter Hunt,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bkoop@uvic.ca
Centre for Biomedical Research, University of Victoria
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                                                                                                                                                                                                                                                                     /Clone_lib="reproductive"
/note="Vector: pBlueScriptIISK+; Library Creator:
Kristlan R von Schalburg ; Atlantic salmon tissue
contributors: Carlo Biagi, Mitch Uh and Robert Devlin (DFO
/Vancouver, B.C.), Simon Jones (PBS, Nanaimo, B.C.),
Seaspring Hatchery (Crofton, B.C.), Rachel Roper
(University of Victoria)"
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/strain="McConnell"
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CDNA preparation, sequencing and bioinformatics:
Y Butterfield, R Kirkpatrick, J Asano, N Girn, R
S Lee, T Olson, P Pandoh, A Prahbu, D Smailus, L
S Taylor, G Yang, J Schein, S Jones and M Marra.
                                                                                                                                                                        BX339684 1201 bp mRNA linear BX339684 Homo sapiens PLACENTA COT 25-NORWALIZED | Clone CSODIO75YB16 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Centre for Biomedical Research University of Victoria PO Box 3020 STN CSC, Victoria PTel: 250 472 4067 Fax: 250 472 4075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GRASP Consortium, Davidson, W.S., Koop, B.F. and http://web.uvic.ca/cbr/grasp.
A survey of Salmo salar transcripts from high complexity cDNA
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                           Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 1201)
Li.W.B., Gruber,C., Jessee,J.
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AW769312.1
EST.
                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hl62a09.xl NCI_CGAP_Col4 Homo sapiens cDNA clone IMAGE:3005752 3' similar to contains Alu repetitive element;contains element MER6 repetitive element; mRNA sequence.
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                                                           High quality sequence stop: 414.
                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                              Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9777.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
a 251 c 310 g 275 t 51 others
/organism="Homo sapiens
                                       Location/Qualifiers
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/clone="CS0DI075YB16"
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/mol_type="mRNA"
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                                     BASE COUNT
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BASE COUNT
ORIGIN
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ORGANISM
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                                                                                                                                                                                                                                High
                                                                                                                                                                                                                                                                                                                                                                       High Throughput Sequencing Center
University of Washington
10 Queen Anne Avenue North, Seat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indiminate, 1 to 509)

1 (Dases 1 to 509)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AQ242919 509 bp DNA linear GSS 03-
HS_2061_Al_E07_MR CIT Approved Human Genomic Sperm Library
sapiens genomic clone Plate=2061 Col=13 Row=I, genomic surv
                                                                                                                                                                                                                                                      Class: BAC ends
                                                                                                                                                                                                                                                                                      Email: jwallace@u.washington.edu
Sequence Tagged Connector
                                                                                                                                                                                                                                                                                                                               Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mahairas GG, Wallace JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       scanning the human genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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57; Conserv
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    177
                                                                                                                                                                                                                              quality sequence stop:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sapiens
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  /note="Organ: sperm; Vector: pBeloBAC11;
E-Coli DH10B"
2 78 c 68 g 184 t 2 other:
                                                                                                    /clone="Plate=2061 Col=13 Row=I"
                                                                                                                          /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
                                                                /clone_
                                                                                   /sex="male"
                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="Organ: colon; Vector: pCMV-SPORT6; Site_1: Sal1;
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.7 kb. Life Technologies catalog #:
11531-019"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3005752"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone_lib="NCI_CGAP_Co14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /tissue_type="moderately-differentiated adenocarcinoma"
/lab_host="DH10B"
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                                        lib="CIT Approved Human Genomic Sperm Library
'Organ: sperm; Vector: pBeloBAC11; BAC Clones i
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Pred. No. 2.6e+02;
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CITBI-E1-2549K13.TR CITBI-E1
     BZ220889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Clones are available from Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Other_GSSs: CITBI-E1-2549K13.TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Use of BAC End Sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: hbe@tigr.org
                                                                                                                                                                                                                                                Similarity
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                                                                                                          GTTAAAAAAACGGTATTTCCCTGGT 91
                                                                                                                                                        ACAGTAATAATTGTTCCAGGCAAGAATTATCAGCGGATGCTAAAACTAATGGGTACAAGT 310
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                                                                                      ATGAAAAACAAGATATTTACATGGT 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primer: M13 Reverse
                                                                                                                                                                                                                                                                                                                     214
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                                                                                                                                                                                                                                                                                                              /cell_type="sperm"
/clone_lib="CITBI-E1"
/note="Vector: pBeloBAC11; Site_1:
CalTech Human BAC Library D"
BO C 87 g 144 t
                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2549Kl3"
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                                                                                                                                                                                                                                                             71 AAAAAACGGTATTTCCCTGGTTCTGATCCAACA 103
                                                                                                                                                                                                                                                                                                                                11 GAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: 271 row: O column: 12 Seg primer: SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                   AGENCOURT_10403096 NIH_MGC_825', mRNA sequence.
BU853968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao bepartment of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CH230-271012.TJB CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-271012, genomic survey sequence.
                Homo sapiens
                                                                                                                                       BU853968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jong,P. and Fraser,C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BZ220889.1 GI:23879247
Eukaryota;
                                Homo sapiens (human)
                                                                   BU853968.1 GI:24038934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clones are derived from the rat BAC library CHORI-230 (http://www.chori.org/bacpac/rat230.htm). For BAC library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Other_GSSs: CH230-271012.TVB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  /Clone_lib="CHORI" 230 Segment 2"
//Clone_lib="CHORI" 230 Segment 2"
//note="Vector: pTARBAC1.3; Site_1: MboI; Site_2:
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produce
Pieter de Jong"
118 c 131 g 252 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-271012"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Rattus norvegicus"
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Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                   29.7%;
58.1%;
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Pred. No. 2.8e.
0; Mismatches
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2.8e+02;
les 39;
                                                                                                                     sapiens
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1e IMAGE:6621037
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H92721/c
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 464)

Hillier,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                          Unpublished
Contact: Wilson RK
                                                                              ,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.
The WashU-Merck EST Project
Washington University School of Medicine
                                                                                                                                                                                                                                          Homo sapiens (human)
                                                                                                                                                                                                                                                                                  EST.
                                                                                                                                                                                                                                                                                                                     IMAGE: 231601
H92721
                                                                                                                                                                                                                                                                                                 H92721.1 GI:1099049
                                                                                                                                                                                                                                                                                                                                                     yt90h01.rl Soares_pineal_gland_N3HPG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLCM2872 row: b column: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 435.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA Library Preparation: CLONTECH Laboratories, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTAATGGTGGGAGTCCCAGCTCATGCATTTCTGAATATACAAAACAGTTTGCAGAAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTTGGCCATTTCAGGT 600
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  (bases 1 to 785)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="PH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_82"
/clone_lib="NIH_MGC_82"
/note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCGACATG-dT(30)BN-3' (where B = A, C, Or G and N = A, C, G, Or T). Average Insert size 1.35 kb (range 0.9-4.0 kb). 14/15 colonies contained inserts by PCR. This library was enriched for full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               clones and was constructed by Clontech Laboratories (Palo
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Pred. No. 2.9e+02;
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Louis, MO 63108
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                                                                                                                                                                                                                                                  Contact: Mark Fredricksen
Department of Plant Biology
University of Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (indica cultivar-group)
Oryza sativa (indica cultivar-group)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BR060006B20E09.abi IRRI clones Oryza sativa (indica cultivar-group) cDNA clone BR060006B20E09.abi similar to NP_180151.1| (NM_128140) unknown protein [Arabidopsis thaliana] gij3643603|gb|AAC42250.1| (AC005395) unknown protein [Arabidopsis thaliana], mRNA sequence.
                                                                                                                                                                                 1201 W. Gregory Dr., Urbana,
Tel: 2172655473
                                                                                                                                                                                                                                                                                                                                                                       Rice Microarray
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 GACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATAC 65
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Bennett, J., Arumugam, K., Lafitte, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA762153.1
                                                                       http://www.iris.irri.org)
                                                                                                         Email: bohnertlab@life.uiuc.edu
International Rice Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 599 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 280.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

13 t 17 others
                                     Location/Qualifiers
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/clone="IMAGE:231601"
/lab_host="DH1DH (ampicillin resistant)"
/clone_lib="Soares_pineal_gland_N3HPG"
/clone_lib="Soares_pineal_gland_vector: pT7T3D (Pharmacia)
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
/note="Organ: pineal gland; Vector: pT7T3D (Pharmacia)
/note="Soares_pineal gland; Vector: pT7T3D (Phar
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/db_xref="GDB:3861592"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
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                                                                                                         System (IRIS,
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/organism="Oryza sativa

(indica

cultivar-group)"

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VERSION
KEYWORDS
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    FEATURES
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Best Local Similarity
                                                                                                                                                                    JOURNAL
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                                                                                                                                                                                                                                                                           Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13
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GSS; genome survey sequence.
Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43;
                Web: www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                               Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Estimate of human gene number provided by using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C. Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
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Eukaryota; Metazoa; Chordata;
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                                                                                                                                                                                                          Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 252F17 of library G from Tetraodon nigroviridis, genomic survey
                                                                                                                                                                                                                                                          10899143
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Panicles"
/dev_stage="Flowering"
/clone_lib="IRRI clones"
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/clone="BR060006B20E09.ab1"
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/cultivar="IR64"
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ORIGIN
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                                                                                                                                                                                                                                                                               source
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                                                                                                                                                                                                                                                                                                                                                                                     www-bio.llnl.gov/bbrp/image/image.html Base Calling / Quality Scores: PHRED from University of Washingtton Genome Center. Vector Trimming: cross_match from University of Washingtion Genome Center PHRAP suite. Poly-T Identification: patMatch.pl from Berkeley Drosophila Genome Project. University of Washingtion.Genome Center: http://www.genome.washington.edu Polyadenylation: Based upon the presence of a XhoI site followed by a run of 14 or more T residues at the beginning of the sequence, this CDNA insert was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6 GACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATAC
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                                                                                                                                                                                                                                                                                                                         Plate: LLCM1 row: D column: 12 High quality sequence stop: 376.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
Tissue Procurement: DCTD/DTP cDNA Library Preparation: Ling
Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E.
Consortium (LINL) DNA Sequencing by: Berkeley MGC sequencing
project Clone distribution: MGC clone distribution information
be found through the I.M.A.G.E. Consortium/LLNLat:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Other_ESTs: 2819291.5prime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA sequence.
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_7"
/clone_lib="NIH_MGC_7"
/clone="Organ: lung; Vector: pOTB7; Site_1: xhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Genoscope sequence ID :
pUC-Ori"
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/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="252F17"
                                                                                                                                            /tissue_type="small cell carcinoma"
/cell_line="MGC3"
                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="G"
                                                                                                                                                                                       /clone="IMAGE:2819291"
                                                                                                                                                                                                                                                         /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Library constructed by Ling Hong

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BASE COUNT
ORIGIN
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BZ153139
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Query Match
Best Local Similarity
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Best Local (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                    (http://www.chori.org/bacpac/or ering_information.htm). BAC end
page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html
Plate: 407 row: 0 column: 5
                                                                                                                                                                                                                                                                                                                                                        Email: szhao@tigr.org
Email: szhao@tigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished Other_GSSs: CH230-40705.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., Jong, P. and Fraser, C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSS
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CH230-40705.TJ CHORI-230 Segment 2 Rattus norvegicus
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47; Conserv
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Fax: 301 838 0208
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                                                              146
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                                                      /Clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1:
/note="Vector: pTARBAC1.3; Site_1:
CHORI-230 Rat (BN/SSNHSd/MCW) BAC 1
Pleter de Jong"
122 c 112 g 214 t
                                                                                                                                                                      /organism-"Rattus norvegicus"
/mol_type-"genomic DNA"
/strain-"BN/SSNHSd/MCW"
/db_xref-"taxon:10116"
/clone-"CH230-40705"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (University of ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)." 76 c 77 g 138 t
                                                                                                                                                            /sex="Female"
                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                          /cell_type="Brain"
                                                                                                                                                                                                                                                          . 594
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29.3%;
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Pred. No. 3
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30.2;
No. 3.
DB 28;
1.6e+02;
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1.4e+02;
1es 28;
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BF358120
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41
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AAGAACATCACTAAAAAGCTCAAGCATAAGGTAAGACCAACAATAGTGGAAAAAACCCTAT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOllveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=MR4&t2=MR4-LT0077-
240500-209-d07&t3=2000-05-24&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shotgun sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Simpson, A.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 317)
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                                                                                  Similarity
AATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAAAAAAACGGTAT 82
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                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           quality sequence stop: 317.
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                                                                                                                                                                                                                              /note="Organ: leiomios; Vector: puc18; Site_1: SmaI; Site_2: SmaI, A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of
                                                                                                                                                                tissue mRNA and cDNA amplification were low stringency conditions."
72 c 42 g 84 t
                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                      /clone_lib="LT0077"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
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                                                                             29.1%;
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                                                                                Score
Pred.
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                                                                                30;
                                                                                DB 10;
3.6e+02;
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                                                                                                 Length 317;
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                                                                                             308
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                                                         67 GTTAAAAAAA 76
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                                                                                                                                                                      45;
                                                                                                                                  7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: +44 131 650 6760
Fax: +44 131 670 5450
Email: mark.blaxter@ed.ac.uk
Sequenced from the Filarial Genome Project's Brugia malayi BAC
library constructed by Jesse Pope-Chappel and Jeremy Foster. The
sequence was generated by The Pathogen Sequencing Unit, The Sanger
Centre, Cambridge, UK in collaboration with Mark Blaxter, ICAPB
,University of Edinburgh, Edinburgh, UK
Seq primer: SP6 (CGCCAAGCTATTTAGGTGACAC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brugia malayi
Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BH002214 382 bp DNA linear BMBAC02E16SP6_PSU Brugia malayi Genomic Bac Library malayi genomic, genomic survey sequence.
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1 (bases 1 to 382)

Whitton,C., Daub,J., Ware,J., Quail,M., Ha,J., Guiliano,D., Slatko,B. and Blaxter,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malay
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Genome survey sequences from the human parasitic nematode Brugia
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                                                                                                                ACTGGAATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACA 66
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                     GTTTAAAAGA 239
                                                                                           ACTTGAATAGAAATTTAAATGGAGAATTTATACTGCGTAGCTAAGTGTATGAATTATACA
                                                                                                                                                                                                                                                              134
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                            /Clone_lib="Brugla malayi Genomic Bac Library 1 & 2"
/note="Vector: pBeloBAC II; Site_1: Hind III; Brugla
malayi genomic DNA was partially cleaved with Hind III and
size fractionated 18,000 clones were generated from 2
libraries with mean insert size 60 kbp. The library was
constructed by Jesse Pope-Chappel, Smith College
                                                                                                                                                                                                                                                                                 M
                                                                                                                                                                                                                                                                                             Northhampton MA and Dr Jeremy Foster, New England Biolabs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            /sex="Mixed (male and female)"
/tissue_type="whole parasite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="TRS"
                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type-"genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Brugia malayi"
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                                                                                                                                                                                   29.1%;
                                                                                                                                                                                                                                                              73 c
                                                                                                                                                                                   Score 30; DB 28;
Pred. No. 3.7e+02;
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1 & 2 Brugia
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AZ460533/c
LOCUS
133 CAGCATTAGATATACATGCATAAATAAATTCCCAATCCAGTTACAACAAAGGCATTGTCG
                                               AZ460533 592 bp DNA linear GSS 04 1M0265H22R Mouse 10kb plasmid UUGC1M library Mus musculus clone UUGC1M0265H22 R, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D.,Weiss,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plate: 0265 row: H column: 22
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mouse whole genome
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               High quality sequence stop: 592.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Erro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (house mouse)
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                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                              was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMDA2 (9i|4732114|9b|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                           chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
1 145 c 111 g 156 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                musculus C57BL/6J (male) was obtained from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. Coli strain XL10-Gold, T1-resistant, F
/clone_lib="Mouse 10kb plasmid UUGClM library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (http://www.jax.org/resources/documents/dnares/). The DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="UUGC1M0265H22"
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67.7%;
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                                                                                                                              Score 30;
Pred. No.
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                                                                                                                                                             DB 28;
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RESULT 45
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VERSION
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BH294981/c
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                                                                                                                                                                   407 AATCAGAGTTAATATATGTTACAAAACTCATATGGATAAGTGATGTGTTTAAAAAGATAA 348
                                                                                                                                     72 AAAAACGGTATTTCCCTGGTTCTGAT 97
                                                                                                                                                                                    12 AATAACAGTTTAATGACAGCATTAATAGCTCCTGCATATGTGAATTGCTAATACAGTTAA 71
AZ496877 688 k
1M0333D03R Mouse 10kb plasmid
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BH294981.1 GT:17207389
GSS.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: szhao@ttigr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BH294981
CH230-186011.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone CH230-186011, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.chori.org/bacpac/or ering_information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 186 row: O column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Riggs, F., o Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 EcoRI segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Shaying Zhao
Department of Eukaryotic Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Other_GSSs: CH230-186011.TV
                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (bases 1 to 612)
                                                                                                                                                                                                                                                                                                                               193
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                                                                                                                                                                                                                                                                                                                         Pieter de Jong"
1 115 c 103 g
                                                                                                                                                                                                                                                                                                                                                  /clone_lib="CHORI-230 Segment 1"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI;
CHORI-230 Rat (BN/SSNHSd/MCW) BAC library produced by
                                                                                                                                                                                                                                                                                                                                                                                                                                             /strain="BN/SsNHsd/MCW"
/db_xref="taxon:10116"
/clone="CH230-186011"
                                                                                                                                                                                                                                                                                                                                                                                                               /cell_type="Brain"
                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Rattus norvegicus"
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Pred. No.
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UUGC1M library Mus musculus
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AUTHORS
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ACCESSION
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377 CAGAAAAAATCTGACTGTCCTTGAGTCTCTTC
                                                   65 CAGTTAAAAAAACGGTATTTCCCTGGTTCTGATC
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Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        clone UUGC1M0333D03 R, genomic survey sequence
AZ496877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Utah Genome Center University of Utah
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AZ496877.1 GI:10673385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 688)
                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil47321.4) gblp4F129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified who shared adaptors to the insert adaptors.
                                                                                                                                                                                                                                                                                                                                                         chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
1 142 c 123 g 231 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                         purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Mouse 10kb plasmid UUGC1M library"
/note="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jack
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Biomedical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="UUGC1M0333D03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:10090"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               hydrodynamically sheared by repeated passage through a 5 inch orifice at constant velocity. The sheared DNA
                                                                                                                                                                                                                                               29.1%;
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Polymers Research Bldg., 20 S. 2030 E., SLC, UT
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Pred. No.
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. 4.2e+02;
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